

**STIC-Biotech/ChemLib**

---

**From:** Slobodyansky, Elizabeth  
**Sent:** Tuesday, November 27, 2001 7:01 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** 09/590,375

Please search for case 09/590,375:

SEQ ID NOs: 1 and 2 against protein, DNA ~~and interference~~ databases.

Thank you.

Elizabeth Slobodyansky, PhD  
Primary Examiner

AU 1652  
CM1-10D11  
tel. 306-3222

**mail box 10C01**

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 11/30/01  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**



```

56 1g1yrglyalatyaspLeutyaspLeuglyglupheasnnglnlysg 73
   ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:
47 .GGGTACGACGCTACGATCTGATGATCGGGCCAGTGTGACCAAG 95
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 1yhrvalargthlytyrglythrarserglnleuglnlyalaval 89
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 GCTCCAAAGCGACAGTGGGCCCAAGACCACTGGACGAGCTGTC 145
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 Thrseryleuysasnnglylllelnvaltyrglyaspvalymets 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
146 CGGCGCGCGGGGACGCCGATGACATCTGTTGATCCGCTGTGAA 195
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
106 nhlsygllygllyalaspLythrglumetvalasnalaval 123
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 CCACAAAGCGCGCGGATTCACCGACGACGAGTCTTCCACGAGG 245
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 sn.Arg..... 124
   |||||
246 ACCGAGAGGTTTGGCCGTGATTTGCCATGGGCAAGATCCGTTGTA 295
   |||||
125 .....Ser 125
   |||||
236 TCGCATCCGCGCTGACAAAGAACTGCCACGATCTTGATGTGCA 345
   |||||
126 AsnArgasnnglnlyleserlygllythrythrllelnalatrptly 142
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
346 GATCCCGCCANACAGTGCATCGCCGGAGAGATCGAGCGCTGACCA 395
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
142 spheasphepseroglyargglyasnThrHisSerAsnphelystrpar 159
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
396 GTTCACATCCAGCGCGCATGATCAATATAGCTCCGCGCGTGCAGCA 445
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
159 rptyrHisphaspelythrasptaspaslnserArglnleuglnasn 175
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
446 AGCGCATTTTACAGGTGTGACATGACAAATGCAACTGT...GAAAG 492
   |||||
176 LyslleTyLyspheargglythrglylsalatrpastrppluvalas 192
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
493 GCCATATGCTTTGTAG.....GGCAGAAAGTGGCGGAGATGTCAA 536
   |||||
192 p1leuglnnglyasnTyraSPtyrLeu..... 201
   |||||
537 CGGGAGCTTTGTAATGACTGACTGTGAGTCTGAGTCTGAGTCTGAG 586
   |||||
202 .....MetyrlAasp 205
   |||||
587 TTTCTGACGCTCCGCGCTAAATTGATGCTATGCAATGTTGCAAGC 636
   |||||
206 1leaspMetAspHisProgluval1leasnnglnleuArgasnTrp 222
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
637 CTAGATCATTCATCTCTGAAGTCAAGAGTCTTAAAGTGCCCAA 686
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
222 1trpTyThrAsnThrleuasnleuaspLyphnearglyleaspval 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:
687 GTGGCTCAAGATCAATGTTGCTGGCGCTTTCGCTGAGCGCGCTTA 736
   |||||
239 yshisile 241
   |||||
737 AAGCATA 744
   |||||
seq_name: gb_est2:BF648578
seq_documentation_block: 665 bp mRNA EST 20-DEC-2000
LOCUS BF648578
DEFINITION NF047G02EC1F019 elicited cell culture Medicago truncatula cDNA
clone NF047G02EC 5', mRNA sequence.
ACCESSION BF648578
VERSION BF648578.1 GI:11913708
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

```

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 665)
AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Iman,J.T., Weller,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
Center for Medicago Genomics Research
JOURNAL Unpublished (2000)
COMMENT Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert length: 665 Std Error: 0.00
plate: 047 row: G column: 02
Seq primer: TCACACGAGAAACAGCTATGAC.
Location/Qualifiers
1. 665
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF047G02EC"
/tissue_type="Elicited cell culture"
/dev_stage="Cell suspensions were derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
BASE COUNT 196 a 131 c 128 g 207 t 3 others
ORIGIN
alignment_scores:
Quality: 202.50 Length: 250
Ratio: 1.594 Gaps: 10
Percent Similarity: 50.800 Percent Identity: 26.400
alignment_block:
US-09-590-375-2 x BF648578 ..
Align seg 1/1 to: BF648578 from: 1 to: 665
13 pheglutprhisleuproasnaspGlyAsnHisrpsasnrgleuargas 29
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 TTCAACTGGGAGTCACGTACCAAGAGAGATGTGACAACTTTGAGAA 136
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
29 paspalalalasnleuysserlysglylethralavaltrp1leprop 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
137 CCTCATTCCTGACCTAGCAATGCTGGAATTACACATGTTGGCTTC 186
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
46 roalatrplysglythrserylnasnspvalyglytyrglyalatyasp 62
|||:|||||:|||||:|||||:|||||:|||||:|||||:
187 CT.....CCATCTCAAGTGTGTGCTCTCAAGATATCTTCAGAGAA 230
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 leutyaspLeuglyglupheasnnglnlysglythrvallargthlysty 79
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
231 CTTTATGATCTTGAT.....GCATCAATA 256
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 rglYthrarserglnleuglnlyalavalThrseryleuysasnng 96
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 CGGTTCAAAGATGACCTAAAGTCACTAATTGACACTTTCAAAGTAAAG 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 1ytlelnvaltyrglyaspvalvalmetasnHislysglyalasp 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
307 GAATCAATGTCTAGTGCATAGATCAACCAT..... 341
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 GlyThrGlumetvalasnalavalgluvalAsnArgSerAsnArgasn 129
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
342 .....AGACAGCAGAAAGAA 358
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```





/db\_xref="taxon:148305"  
 /clone\_id="CUG1 Rice Blast BAC Library"  
 /tissue\_type="Protoplasts"  
 /lab\_host="E. coli DH10B"  
 /note="Vector: pBACWICH; Site\_1: HindIII; Site\_2: HindIII;  
 Rice blast is one of the most devastating fungal diseases  
 of rice world wide. It is a filamentous ascomycete with  
 a haploid genome (n=7) of approximately 40 Mbp. Rice  
 blast is an important model fungal pathogen for studying  
 numerous aspects of the fungal-host interaction. In  
 order to facilitate genome wide analysis, a BAC library  
 containing 9216 clones with an average insert size of 130  
 kbp was constructed. This library represents greater  
 than 25x genome coverage. High density colony filters  
 are available upon request."  
 BASE COUNT 120 a 226 c 222 g 126 t  
 ORIGIN

alignment\_scores:  
 Quality: 198.00 Length: 155  
 Ratio: 2.041 Gaps: 7  
 Percent Similarity: 62.581 Percent Identity: 36.129

alignment\_block:  
 US-09-590-375-2 x AQ159867 ..

Align seg 1/1 to: AQ159867 from: 1 to: 694

```

344 ValGlnSerTrpPheLysProLeuAlaTyrAlaLeuLeuThrAla.. 359
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
150 GTAGAACCTCTCTCATCCGATCGCTACGCGCTGATCCTCCTCGCGC 199
360 .GlunGlnGlyTyrProSerValPheTyrGlyAspTyrGly.....I 374
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
200 TAAACACGCGACGCGCTGCTCTGTCGACCTGACGCGACGCTGCTG 249
374 LeProThrHisGlyValProSerMetLysSerLysIle.....AsPro 388
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
250 TGGCGTTCGCGCGCGCGCGCGCGCGCGCGCTGCTGACGCGCGG 299
389 LeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThrGlnHisAspTyr 405
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
300 CTATGCTGCGCGCGACGCTGCTGCGGCTACGCGACGCGCGCTACT 349
405 e.....AspHisHisAspIleLeuGlyTyrThrArgGlnGlyAsp 419
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
350 TTGCGGACAGGCGCGCGACGCTGCTGCGCTGCGCTTCGCGC.... 395
419 eSerHisPro.....AsnSerGlyLeuAlaThrIleMetSer 431
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
396 .....CACCGCGCGCGCTCGCGCGCGCGCGCTGCGCGCGCAC 440
432 AspGly...ProGlyGlyAsnLysTyrMetTyrValGlyHisLysAl 447
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
441 ACGGCTTCGAGCGCGCGCGCGCGCATGCTGCGGTCGCGCATGCG 490
447 aglyGlnValTrpArgAspIleThrGlyAsnArgSerGlyTyrValThr 464
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
491 CGGCGAGCGCTGACCGACGCTGCTCGCGCGCATGCTGCGGCTCG 540
464 LeuAsnAlaAspGlyTyrPheLysAsnThrValAsnGlyAlaValSer 480
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
541 TCGACGCGCGCGGCTACGCGAGTTCCGTCGTCGCCAGGCGGCTACG 590
481 ValTrpValLysGln 485
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
591 GTTGGGTCCACGAG 605
seq_name: gb_est2:BG581061
seq_documentation_block:

```

LOCUS BG581061 558 bp mRNA EST 11-APR-2001  
 DEFINITION EST482791 GVN Medicago truncatula cDNA clone pcvN-63M12 5' end,  
 mRNA sequence.  
 ACCESSION BG581061  
 VERSION BG581061.1 GI:13596125  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eustroids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.

REFERENCE 1 (bases 1 to 558)  
 Pedrovic, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Town  
 C.D., Van Aken, S., Utterback, T., Cho, J., and Fraser, C.M.  
 ESTs from one month old nitrogen-fixing root nodules of Medicago  
 truncatula, 2001  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Carroll P. Vance  
 Department of Agronomy and Plant Genetics  
 University of Minnesota  
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA  
 Tel: 612 625 5715  
 Fax: 651-649-5058  
 Email: Vance004@maroon.tc.umn.edu  
 University of Minnesota name: M382117e TIGR sequence name:  
 M382117e More information is available at: <http://www.medicago.org>  
 Seq primer: SKmod (CTA gaa cta gta gta CC).  
 Location/Qualifiers

FEATURES:  
 source

1..558  
 /organism="Medicago truncatula"  
 /cultivar="genotype A17"  
 /db\_xref="taxon:3880"  
 /clone="pcvN-63M12"  
 /clone\_id="GVN"  
 /tissue\_type="N2-fixing root nodules"  
 /dev\_stage="effective root nodules harvested one month  
 post inoculation with Sinorhizobium meliloti"  
 /lab\_host="E. coli strain XL04"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI; cDNA was prepared from polyA+ enriched RNA from  
 effective root nodules harvested one month post  
 inoculation with Sinorhizobium meliloti. The cDNA was  
 directionally ligated into the Uni-ZAP XR vector from  
 Stratagene and packaged using cDNA inserts were excised  
 from the recombinant lambda-ZAP phage using Ex-Assist  
 helper phage and propagated in XL04 cells."  
 BASE COUNT 169 a 110 c 115 g 163 t 1 others  
 ORIGIN

alignment\_scores:  
 Quality: 197.00 Length: 230  
 Ratio: 1.684 Gaps: 8  
 Percent Similarity: 50.870 Percent Identity: 26.522

alignment\_block:  
 US-09-590-375-2 x BG581061 ..

Align seg 1/1 to: BG581061 from: 1 to: 558

```

9 MetMetGlnTyrPheGlnTrpHisLeuProAsnAspGlyAsnHisTyr 25
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
25 CTTCTTACGAGGATTCACGTCGAGGATCAAGTAACAAGAGGATGTACA 74
25 nargLeuArgAspAspAlaAlaLeuLysSerLysGlyIleThrAla 42
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
75 CTCCTTGAGAACCTCATCTCGACCTAGCAAAATGCGAATTACACATG 124
42 attTrpLeuProAlaTrpLysGlyThrSerGlnAsnAspValGlyTyr 58
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
125 TTGGGCTCTCTCT.....CCATCTCAAAAGTTGCTGCTCAAGGATAT 168

```

```

59 g1a1a1yAspLeuTyRAspLeuGlyGluPheAsnGlnLysGlyThrVa 75
169 CTCACAGAAAGACTTATGATCTTGAT..... 195
75 lArgThrLysTyRgLyThrArgSerGlnLeuGlnclValAlaValThrSerL 92
196 .GCATCAAAATACGGTTCMAAAGATGACCTAAAGCTAAATTCAGAGCTT 244
92 euLysAsnAsnGlnLylleGlnValTyRgLYAspValValMetAsnHisLys 108
245 TCMAAGATTAAGAAAGATCAATGTCAGTACATGATGTCACCAAT... 291
109 G1yG1yAlaAspGlyThrgLumetValAsnAlaValGluValAsnArgSe 125
292 .....AGAAC 296
125 rAsnArgAsnGlnGluLleSerGlyGluTyThrllleGlnAlaThrPThrL 142
297 AGCAGAAAGAAAGATGATAGAGCATCTATTCCTC..... 333
142 ySPheAspPheProGlyArgGlyAsnThrHisSerAsnPhelystrrParg 158
334 .....TTTGAAGGT...GGGACTCCTGATTCAAACTT..... 363
159 TrpTyRHisPheAspGlyThrAspTrpAspGlnSerArgGlnLeuGlnAs 175
364 .....GATTGGGGCCCATCTTCATTTGCAAGA 392
175 nLyslleTyRlysPheArgGlyThrgLyLysAlaThrpsrTrpGluVala 192
393 TGACACACTGCTTATTCAGATGCACATGCA.....A 421
192 sPllleGluAsnGlnLysAsnTyRAspTyRLeuMetTyRAlaAspIleAspMet 208
422 ACCTGATAGTGGAGAG...GGCTATCAAGCTGCACCTGACATTCATCAT 468
209 AspHisPProGluValIleAsnGlnLeuArgAsnTrpGlyValTrpTyRTh 225
469 CTCATTCCTCAAGTACAAAAGATGATCTGAATGATGATGATGCTCA 518
225 rAsnThrLeuAsnLeuAspGlyPheArgIleAspAlaVal 238
519 AACTGAAATGTGATTTCTGTTGGAGATTGATTTTGTG 558
seq_name: gb_est2:BF637944
seq_documentation_block:
LOCUS BF637944 587 bp mRNA EST 19-DEC-2000
DEFINITION NF041C08PLF1056 Phosphate starved leaf Medicago truncatula cDNA
clone NF041C08PL 5', mRNA sequence.
ACCESSION BF637944
VERSION BF637944.1 GI:11902102
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eucosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 587)
REFERENCE 1 (bases 1 to 587)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
H.R., Iman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org

```

```

Insert Length: 587 Std Error: 0.00
Plate: 041 row: C column: 08
Seq primer: TCACAGAAAGAAAGACGATGATC.
FEATURES
source
1..587
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF041C08PL"
/clone_lib="Phosphate starved leaf"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 200m potassium phosphate. RNA was prepared from above ground tissues."
BASE COUNT 172 a 117 c 119 g 179 t
ORIGIN
alignment_scores:
Quality: 196.00 Length: 228
Ratio: 1.675 Gaps: 8
Percent Similarity: 51.316 Percent Identity: 26.316
alignment_block:
us-09-590-375-2 x BF637944 ..
Align seg 1/1 to: BF637944 from: 1 to: 587
9 MetMetGlnTyRPhelGluThrHisLeuProAsnAspGlyAsnHisTrpAs 25
59 CTTCTTCAGGGAFTCACTCGGAGATCAAGTACAAAGAGATGGGTACAA 108
25 nArgLeuArgAspAlaAlaAsnLeuLysSerLysGlyIleThrAlaVal 42
109 CTTCTTGAAGAACCTCATCTCGACCTAGCAAAATCTGGAAATTAACACATG 158
42 aTrpIleProAlaThrPlyLysGlyThrSerGlnAsnAspAlaGlyTr 58
159 TTTGGCTTCCTCTCT...CCATCTCAAAAGTGTGGTCTTCAAGAGAT 202
59 G1yAla1yAspLeuTyRAspLeuGlyGluPheAsnGlnLysGlyThrVa 75
203 CTCACAGAAAGACTTATGATCTTGAT..... 229
75 lArgThrLysTyRgLyThrArgSerGlnLeuGlnclValAlaValThrSerL 92
230 .GCATCAAAATACGGTTCMAAAGATGACCTAAAGCTAAATTCAGAGCTT 278
92 euLysAsnAsnGlnLylleGlnValTyRgLYAspValValMetAsnHisLys 108
279 TCMAAGATTAAGAAAGATCAATGTCAGTACATGATGTCACCAAT... 325
109 G1yG1yAlaAspGlyThrgLumetValAsnAlaValGluValAsnArgSe 125
326 .....AGAAC 330
125 rAsnArgAsnGlnGluLleSerGlyGluTyThrllleGlnAlaThrPThrL 142
331 AGCAGAAAGAAAGATGATAGAGCATCTATTCCTC..... 367
142 ySPheAspPheProGlyArgGlyAsnThrHisSerAsnPhelystrrParg 158
368 .....TTTGAAGGT...GGGACTCCTGATTCAAACTT..... 397
159 TrpTyRHisPheAspGlyThrAspTrpAspGlnSerArgGlnLeuGlnAs 175
398 .....GATTGGGGCCCATCTTCATTTGCAAGA 426
175 nLyslleTyRlysPheArgGlyThrgLyLysAlaThrpsrTrpGluVala 192

```

```

427 TGACACTGCTTATTTCAGANGCAGCTGGA.....A 455
192 spilegiuasnglyasntryasptryleumetyrilaaspilaspmet 208
   :|||||:|||||:|||||:|||||:|||||:|||||:
456 ACCTCGATAGTGAGAG...GGCTATCAAGCTGCACCTGCATGTGATCAT 502
209 Asphisprogluvalileasngluleuargasntrpilyaltrpyrth 225
   :|||||:|||||:|||||:|||||:|||||:|||||:
503 CTCATCTCCTCAAGTACAAAAGAGTATCTGAATGATGATGGCTCAA 552
225 rASNThleuasnlleuaspglypheargileasp 236
   :|||||:|||||:|||||:|||||:|||||:|||||:
553 AACTGAATTTGATTTCTGCTTGAGATTTGAT 586

seq_name: gb_est2:BF632036

seq_documentation_block:
LOCUS   BF632036      639 bp      mRNA      EST      19-DEC-2000
DEFINITION   NF016C06DTJ1039 Drought Medicago truncatula cDNA clone NF016C06DT
5', mRNA sequence.
ACCESSION   BF632036
VERSION     BF632036.1  GI:11896194
KEYWORDS
SOURCE      EST.
ORGANISM    bairel medic.
            Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1 (bases 1 to 639)
AUTHORS    Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
            Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula drought library
            Unpublished (2000)
JOURNAL
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 639 Std Error: 0.00
            Plate: 016 Row: C Column: 06
            Seq primer: TCACACAGCAACAGCTTATGAC.
FEATURES
source      1..639
            /organism="Medicago truncatula"
            /db_xref="taxon:3880"
            /clone="NF016C06DT"
            /clone_lib="Drought"
            /tissue_type="Plantlets"
            /dev_stage="Pooled timepoints"
            /note="Vector: Lambda Zap; Contains a mixture of entire
            plantlets harvested in a series of days-post-watering
            timepoints."
BASE COUNT   187 a      127 c      126 g      199 t
ORIGIN
alignment_scores:
Quality: 196.00      Length: 240
Ratio: 1.607          Gaps: 9
Percent Similarity: 50.833      Percent Identity: 27.083

alignment_block:
US-09-590-375-2 x BF632036 ..
Align seg 1/1 to: BF632036 from: 1 to: 639
9 MetMeGIntYrPhagLTrPhisLeuPProAsnAspGlyAsnHisTrpAs 25
   :|||||:|||||:|||||:|||||:|||||:|||||:
76 CTCCTTCAGGAGTTCACATGGAGTCAGTACAAAGGAGGATGCTACAA 125

```

```

25 nargleuargaspaspalaalaasnleuysSerlysglyilethralav 42
   :|||||:|||||:|||||:|||||:|||||:|||||:
126 CTCCTTGAAGAACTCATCTCCAGCTACGAAAGCTGATTAACACATG 175
42 aLTrpLleProProAlaLTrpLysGlyThrSerGlnAsnAspValGlyTr 58
   :|||||:|||||:|||||:|||||:|||||:|||||:
176 TTGGCTTCCTCT....CCATCTCAAGCTGTGGCTCCAGAGATAT 219
59 gLyAlaTrAspLeuTyTrAspLeuGlyLubPheasnGlnLysGlyThrVa 75
   :|||||:|||||:|||||:|||||:|||||:|||||:
220 CTCACGAGACCTTATGATCTTGAT..... 246
75 lArgThrLysTyTrGlyThrArgSerGlnLeuGlnGlyAlaValThrSerL 92
   :|||||:|||||:|||||:|||||:|||||:|||||:
247 .GCATCAAAATAGCGTCAAAAGATGACCTTAAGCTATATTCAGCCTT 295
92 euLysAsnAsnGlyLleGlnValTyTrGlyAspValAlaMetAsnHisLys 108
   :|||||:|||||:|||||:|||||:|||||:|||||:
296 TCAGAGATTAAGGAATCATCTGCTAGCTGACATAGTATCAACCAT... 342
109 gLyGlyAlaAspGlyThrGluMetValAsnAlaValGluValAsnArgSe 125
   :|||||:|||||:|||||:|||||:|||||:|||||:
343 .....AGAAC 347
125 rASNargasnGlnGluLleSerGlyLutTyTrThrLleGluAlaTrpThrL 142
   :|||||:|||||:|||||:|||||:|||||:|||||:
348 AGCAGAAAGAAAGATGATAGAGGATCTATTCCTC..... 384
142 yspPheaspPheProGlyArgGlyAsnThrHisSerAsnPhelystrParg 158
   :|||||:|||||:|||||:|||||:|||||:|||||:
385 .....TTTGAAGT...GGACTCCGATTCAAAACTT..... 414
159 TrpTyHisPheaspGlyThrAspTrpAspGlnSerArgGlnLeuGlnAs 175
   :|||||:|||||:|||||:|||||:|||||:|||||:
415 .....GATTGGGGCCCATCTTTCATTTGCAAGGA 443
175 nLysLleTyLysPheargGlyThrGlyLysAlaTrpAspTrpGluValA 192
   :|||||:|||||:|||||:|||||:|||||:|||||:
444 TGACACTGCTTATTTCAGATGCGACTGGA.....A 472
192 spilegiuasnglyasntryasptryleumetyrilaaspilaspmet 208
   :|||||:|||||:|||||:|||||:|||||:|||||:
473 ACCTCGATAGTGAGAG...GGCTATCAAGCTGCACCTGCATGTGATCAT 519
209 Asphisprogluvalileasngluleuargasntrpilyaltrpyrth 225
   :|||||:|||||:|||||:|||||:|||||:|||||:
520 CTCATCTCCTCAAGTACAAAAGAGTATCTGAATGATGATGGCTCAA 569
225 rASNThleuasnlleuaspglypheargileaspalaalaValLysHisLle 241
   :|||||:|||||:|||||:|||||:|||||:|||||:
570 AACTGAATTTGATTTCTGCTTGAGATTTGATTTGCAAGGTTAT 619
242 LysTySerTyTrArg 247
   :|||||:|||||:|||||:|||||:|||||:|||||:
620 GCGCCTAGCATTAACAAA 637

seq_name: gb_est2:BF647599

seq_documentation_block:
LOCUS   BF647599      635 bp      mRNA      EST      20-DEC-2000
DEFINITION   NF077E12C1P1036 Elicited cell culture. Medicago truncatula cDNA
clone NF077E12C 5', mRNA sequence.
ACCESSION   BF647599
VERSION     BF647599.1  GI:11912729
KEYWORDS
SOURCE      EST.
ORGANISM    bairel medic.
            Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1 (bases 1 to 635)

```

**AUTHORS** Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.  
**TITLE** Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Dixon RA  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7302  
 Fax: 580 221 7380

Email: radixon@noble.org  
 Insert Length: 635 Std Error: 0.00  
 Plate: 077 row: E column: 12  
 Seq primer: TCACACGGAACACGCTATGAC.  
 Location/Qualifiers

**FEATURES**  
 source  
 1..635  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF07E12EC"  
 /clone\_lib="Elicited cell culture"  
 /tissue\_type="Cell cultures derived from root tissues"  
 /dev\_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"  
 /note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

**BASE COUNT** 183 a 129 c 125 g 197 t 1 others  
**ORIGIN**

**alignment\_scores:**  
 Quality: 195.00 Length: 232  
 Ratio: 1.681 Gaps: 8  
 Percent similarity: 50.000 Percent identity: 26.724

**alignment\_block:**  
 US-09-590-375-2 x BF647599 ..

Align seg 1/1 to: BF647599 from: 1 to: 635

```

15 TRPHISLEPProAsnspGLyAsnHsrPAsnArgLeuArgAspAspAl 31
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
95 TCGGAGCTCAAGTACAAAGAGAGATGCTGCACTCTTTCAACACCTCAT 144
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
31 aAlAsnLeuLysSerLysGlyLeThrAlaValTrpIleProAlaT 48
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
145 TCCTGACCTAGCAATGCTGGAATTACATGTTGGCTTCCTCT 190
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
48 rPLyGlyThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyr 64
||| ||| ||||| ||||| ||||| ||||| ||||| |||||
191 ..CCATCTCAAAAGTGTGCTCTCAAGGATATCTCCAGGAAGACTTAT 238
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
65 ASPLenGlyLupheAsnGlnLysGlyThrValArgThrLysTyrGlyTh 81
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
239 GATCTTGAT.....GCATCAAAATACGGTTC 264
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
81 rARGSerGlnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleG 98
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
265 AAAAGATGACCTAAAGTCACTATTGCACTTCAAAAGATAAGGATCA 314
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
98 lNValTyrGlyAspValAlaMetAsnHisLysGlyAlaLaspGlyThr 114
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
315 ATTGCTTACTGACATAGTATCAACCAT..... 343
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
115 GluMetValAsnAlaValGluValAsnArgSerAsnArgAsnGlnGlu 131
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
344 .....AGACACGACGAAAGAAAGATGCA 366
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
131 eSerGlyGlyTyrThrIleGluAlaTTrpThrLysPheAspPheProGly 148
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

367 TAGAGCATCTATTCCTC.....TTGAGGT. 394
148 rGGLyAsnThrHisSerAsnPhelySTrPArGTrpTyrHisPheSpGly 164
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
395 ..GGGACTCTGATTCAAACTT..... 415
165 ThrASPTrpAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheAr 181
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
416 ...GATGGGCCCATCTTTCATTTCGAAAGATGACACGCTATTATTCAGA 462
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
463 TGGCACTGA.....AACCTGATTCGAGAG. 490
198 YrASPTrpLeuMetYrAlaAspIleAspMetAspHisProGluValIle 214
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
491 ..GGCTATTCACCTGCACCTGACATTGATCATCTCAATCTCAACTACA 538
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
215 AsnGluLeuArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuS 231
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
539 AAAGACTTATCTGATGATGATGATGATGCTCAAAACGAAATTCGATTTC 588
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
231 pGlyPheArgIleAspAlaValLysHisIleLysTyrSerTyrThr 246
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
589 TCGTTGAGATTTGATTGTTTTCAAANGTATGCGCTACCATATACA 634
||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
seq_name: gb_est2:BF011027

```

seq\_documentation\_block: 771 bp mRNA EST 06-OCT-2000  
 LOCUS BF011027  
 DEFINITION SB233 Sugar Beet germination cDNA library Beta vulgaris cDNA clone  
 YS016f79.5' similar to alpha amylase, mRNA sequence.  
 ACCESSION BF011027  
 VERSION BF011027.1 GI:10711301  
 KEYWORDS EST.  
 SOURCE Beta vulgaris.  
 ORGANISM Beta vulgaris.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.  
 1 (bases 1 to 771)  
 de los Reyes, B.G., McGrath, J.M., Myers, S. and Derrico, C.  
 Differential gene expression in sugar beet seedlings (Beta vulgaris  
 ) germinated under stress conditions  
 Unpublished (2000)  
 Contact: J. Mitchell McGrath  
 Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research  
 Unit  
 Michigan State University  
 494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA  
 Tel: (517)-432-2355  
 Fax: (517)-337-6782  
 Email: mitchmcg@pilot.msu.edu  
 Seq primer: T3  
 High quality sequence stop: 750.

**JOURNAL**  
 COMMENT

**FEATURES**  
 source

1..771  
 Location/Qualifiers  
 /organism="Beta vulgaris"  
 /cultivar="USH20"  
 /db\_xref="taxon:161934"  
 /clone="ys016f79"  
 /clone\_lib="Sugar Beet germination cDNA library"  
 /tissue\_type="whole seedlings"  
 /dev\_stage="4-day germination under stress (salt/NaCl, denaturation/Mannitol and anaerobic stress)"  
 /lab\_host="SOLR"  
 /note="Organ: seeds; Vector: pBluescript II KS (+) excised from Lambda Uni-Zap XR; Site.1: EcoRI; Site.2: XhoI; cDNAs were derived from reverse transcription of pooled mRNA samples from stressed seedlings (germinated for 4 days in 150mM NaCl, 200mM Mannitol, submerged in distilled water and 0.3% Hydrogen peroxide). The cDNA library was generated by directional ligation of the cDNAs in the



```

6 AsnGlyThrMetMetIlnTrpNegIuTrpHisIleProAsnaspGlyAs 22
||| |||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ::
373 AACGAGACCCCTCTTTCAAGCCTTGTAGTGAGCACCTCCCGCGACAAAGC 422
22 nhIstIrrPaenArgLeuArgAspAspAlaIalaSnLeuLysSerLysGlyI 39
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
423 TCACGTGCCTCGACACTCATCTCATATACCACAGCCTTGGCTCTTTGGGA 472
39 IeThrAlaValTrpIleProProAlaTrpLysGlyThrSer..... 52
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
473 TCACCAAGCTMTGGARCCACCGCCTCGAAGGCGCGGTGGTCCTGG 522
53 GlnAspValValGlyTrpGlyAlaTrpAspLeuTrpAspLeuGluIleP 69
:::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
523 AGCAAC..... GGCTACGACGCTGTACGATCTGTATGATGTGGCCAATT 566
69 eaSngInLysGlyThrValArg.....ThrLysTryGlyTr 81
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
567 TGACCGAGAGGGCTCCAGNGCGACCAAGTGGGCCCGACGACCAACAGGAC 616
81 hArgSerIlnLeuGInGlyAlaValThrSerLeuLysasnSngIle 97
::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
617 GAGCTCGTTCCGCGCCGCGGGGAGACCCGCA.....TTT 651
98 GlnValTrpGlyAspValValMetAsnHisLysGly 110
:::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
652 GAGATCCTCTTTGATGCCGTGTAACAACAGNAGCGCGG 690
seq_name: gb_est2:B10733204
```

```

FEATURES
source
seq_documentation_block:
LOCUS      B10733204      702 bp      EST
DEFINITION      P122B.G10 Sugar Beet germination cDNA library Beta vulgaris cDNA 5
VERSION      B10733204
KEYWORDS      similar to alpha amylase, mRNA sequence.
ACCESSION      B1073204.1  GI:14493824
SOURCE      EST.
ORGANISM      Beta vulgaris.
              Beta vulgaris
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
TITLE      1 (bases 1 to 702)
              de los Reyes,B.G., McGrath,J.M. and Myers,S.
              Differential gene expression in sugar beet seedlings (Beta vulgaris
              ) germinated under stress conditions (de los Reyes,B.G., McGrath
              ,J.M., Myers,S.)
JOURNAL      unpublished (2001)
COMMENT      Contact: J. Mitchell McGrath
              Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research
              Unit
              Michigan State University
              494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
              Tel.: (517)-432-2355
              Fax: (517)-337-6782
              Email: mtchmcg@pilot.msu.edu
              Seq primer: T3.
              Location/Qualifiers
              1..702

```

```

/organism="Beta vulgaris"
/cultivar="USH20"
/db_xref="taxon:161934"
/clome_lib="Sugar Beet germination cDNA library"
/tissue_type="Whole seedlings"
/dev_stage="4-day germination under stress (salt/NaCl,
dehydration/Mannitol and anaerobic stress)"
/lab_host="SOLR"
/ncbi:"Organ: seeds; Vector: pBluescript II KS (+) excised
from lambda Uni-zap XR; Site: 1: EcoRI; Site 2: XhoI; cDNA
were derived from reverse transcription of pooled mRNA
samples from stressed seedlings (germinated for 4 days in
150mM NaCl, 200mM Mannitol, submerged in distilled water
and 0.3% Hydrogen peroxide). The cDNA library was

```

generated by directional ligation of the cDNAs in the  
EcoRI and XhoI sites of lambda Uni-zap XR vector  
(Stratagene). The library was excised as a plasmid  
plasmid from lambda Uni-zap XR by Exassist helper phage  
and plated on SOLR host cells.

alignment_scores:		
Quality:	181.50	Length: 247
Ratio:	1.555	Gaps: 9
Percent Similarity:	48.178	Percent Identity: 25.506
alignment_block:		
US-09-590-375-2 x B1073204	..	
Align seg 1/1 to: B1073204	from: 1	to: 702

Align seg 1/1 to: BI073204 from: 1 to: 702

```

9 MetMetClnIytrPheGluTrpHisLeuProAsn...AspGlyAsnHisIstr 24
   :::::||||| ||:::|||||::: ||| ||::: ||| :::
113 TTGTTTCAGGGCTTTCAAATGGGAATCATGCACAACAACGGAGGATTGTA 162
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
24 PAsnArgLeuAtrGAspAspAlaAlaAsnLeuLysSerLysGlyIleThra 41
   ::||| ||:::|||||::: ||::: ||| ||::: ||| :::
163 TAATTCACGTGAACAAATCATGCATGATTTGGCTAGAGCAGGGATTACAC 212
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
41 LaValTrpIleProProAlaTrpLysGlyThrSerGlnAsnAspValGly 57
   |||||:::|||||::: ||::: ||| ||::: ||| :::
213 ATGTTTGGCTTCCCTCCACCAACATCATTTGGTTCTTCCTCA.....GGA 256
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
58 TyGlyAlaIaTrpAspLeuTrpAspLeuGlyLuphAsnGlnLysGlyTh 74
   |||||:::|||||::: ||::: ||| ||::: ||| :::
257 TATCTTCCTGGACAGATTGATGATCTTCAT..... 286
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
74 rValArgTrhLysTyGlyThrArgSerGlnLeuGlnIaValaValThrs 91
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
287 ...GCATCTAGATATGGCAACGGGCGTGAATTAAAGACCTGATTAAAG 332
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
91 erLeuLysAsnAsnGlyIleGlnValTyGlyAspValaValMetAsnHis 107
   ::::: ||:::|||||::: ||::: ||| ||::: ||| :::
333 CCTTCCACCAAAAAGAAATCAAAATGTTGGCGATATACGTAAATCAT 382
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
108 LysGlyLysAlaAspGlyThrGluMetValAsnAlaValGluValAsnAr 124
   ::::: ||:::|||||::: ||::: ||| ||::: ||| :::
383 .....AG 384
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
124 gSerAsnArgAsnGlnIuIleSerGlyGluTrpTrhIleGluAlaTrp 141
   ||| ||::: ||| ||::: ||| :::
385 ATGGCGCAGATPAGCAGACAGTGGTAGCGGAATCTAATCTGATA..... 424
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
141 hrLysPheAspPheProGlyArgGlyAsnThrHisSerAsnPhelyStrp 157
   ||| ||| ||::: ||| ||::: ||| :::
425 .....TTTGAAGCT...GGAATCCAGACAGATGGCCTAGATTTGG 460
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
158 ArgTrpTrhHisPheAspGlyThrasPrpAspGlnSerArgGlnLeuG 174
   ||| ||::: ||| ||::: ||| :::
461 .....GGGCCATCGGCTAATTTGCCAGCGAT..... 484
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
174 pAsnLysIleTrpLysPheArgGlyThrGlyLysAlaTrpAspTrpGluV 190
   ||| ||::: ||| ||::: ||| :::
485 .....GACACTCAAT 494
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
191 aLaspIleGluAsnGlyAsnTyTrAsp.....TyrIleMetTytr 203
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
495 ACCTGTACGAGTACGGGAATCTAGACACTGGACGCTGATGTGTGTCCGA 544
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
204 AlaAspIleAspMetAspHisProGluValAlleAsnGluLeuAtrgAsnTr 220
   ||||| ||::: ||| ||::: ||| :::
545 CCGCATATPACCTCTTAATCCAGAGGTACAAGACAGACTAGTTGATTG 594
   :::|||||::: ||:::|||||::: ||| ||::: ||| :::
220 pGlyValaTrpTrpTrhAsnThrLeuAsnLeuAspGlyPheArgIleAspA 237
   ||| ||::: ||| ||::: ||| :::

```





```

/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEN12E8"
/clone_lib="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; Supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."

```

```

BASE COUNT      183 a      118 c      183 g      194 t
ORIGIN

```

```

alignment_scores:
    Quality: 175.00      Length: 212
    Ratio: 1.577      Gaps: 9
    Percent Similarity: 52.358      Percent Identity: 28.302

```

```

alignment_block:
US-09-590-375-2 x AW223546 ..

```

```

Align seg 1/1 to: AW223546 from: 1 to: 678

```

```

207 AspNetaspriisproglu.....ValileasngluLeuAArgAsnTTPcl 221
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2 AACATTGATCATTTCCAGGAATTCGTGAAGAAGATATCAGGAATGCTT 51
221 yAlaTTPryTThraAnThLeuAsnLeuAspLylphearqileaspaLay 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 ACTGCGCTGAGGAGAGAGATTGTTATGATGATGAGAGCTTGATTGTTG 101
238 allYnHisileLysTyrSerTyrThraGAspTTPLeThraHisValArg 254
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
102 TTCGGGGGTTGGGGGGTGTATGTAAGGATTACTTG..... 139
255 AsnThTThGlyLysPromePheAlaValAlaGluPheTTPlysAsn.. 270
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
140 ..GAAGCAACTGAACCTTACTTCGCTGAGCGAGTTTGGGATTCCCT 186
271 .....AspleuAlaA 274
187 CGTTTAACTTATGAGAGATGATCACAATGACAAGATGCGATAGGCGAGA 236
274 lailegluAsnTyrLeuAsnLysTThraSerTTPAsnHisSerValPheAsp 290
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
237 GAATTAATTCAGCTGATTAATGCTACTAATGAGAACTGCAAGACATTTCAC 286
291 ValPProLeuHisTyrAsnLeuTyrAsnAlaSerAsnSerGlyLysTTPrh 307
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
287 GTGACACAGCAAGGAAATTCCTCATCTCGCAATTCAGAGATGCAATCTAG 336
307 e.....AspMetArgAsnLileuAsnGlySerValAlaGlnLysH 321
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
337 GCGACTATCCGATCGAAGGGGAAACCTCCGCG...GTTGTTGATGGT 383
321 lsrProlleHisAlaValThraPheValAspAsnHisAspSerGlnProGly 337
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
384 GGCACATTCGCTGCTTACATTATAGAGAAATCATGATACAGTTCTACA 433
338 GluAlaLeuGluSerPheValGlnSerTTPrhLysPro..... 350
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
434 CAGGCT.....CATTCGAGATTTCCTGGTGGGGAAGA 465
351 ...LeuAlaTyrAlaLeuLileuThraArgGlnGlnGlyTyrProSerV 366
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
466 GATGCAGAGGTATGCTTATCTCTGACT...CACCCGTGAGACCCGCTCAG 512

```

```

366 alphaTyrGlyAspTyrTyrGlyIleProThraHisGlyValProSerMet 382
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
513 TCTTCTTT.....GATCACATTTTCTCTGCTTAC 541
383 LysSerLysIleAspProLeuLeuGlnAlaArgGln 394
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
542 CGATCTGAATAGGAATCTTTATCATCTACACAGAAG 577

```

```

seq_name: gb_gss:CNS0001B

```

```

seq_documentation_block:

```

```

LOCUS

```

```

CNS0001B

```

```

456 bp

```

```

DNA

```

```

GSS

```

```

28-JUN-1999

```

```

Arabidopsis thaliana genome survey sequence SP6 end of BAC T7A19 of
TAMU library from strain Columbia of Arabidopsis thaliana, genomic
survey sequence.

```

```

ACCESSION

```

```

AL091025

```

```

AL091025.1

```

```

GI:5292179

```

```

VERSION

```

```

KEYWORDS

```

```

SOURCE

```

```

ORGANISM

```

```

Arabidopsis thaliana

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 456)
Salanoubat,M., Choisme,N., Artiguenave,F., Brothier,P., Mincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Queller,F.
Unpublished
2 (bases 1 to 456)
Genoscope.
Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequence :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
1..456
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="TAMU"
/clone="T7A19"
/note="end : SP6"
BASE COUNT      128 a      112 c      88 g      128 t
ORIGIN

```

```

alignment_scores:

```

```

Quality: 173.50

```

```

Ratio: 3.402

```

```

Percent Similarity: 77.273

```

```

Percent Identity: 48.485

```

```

alignment_block:
US-09-590-375-2 x CNS0001B ..

```

```

Align seg 1/1 to: CNS0001B from: 1 to: 456

```

```

6 AsnglyThmelmecGlnTyrPheGluTTPrhLysleProAsnAspLys 22
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
259 AACCTCACACCTCTTCAATCTTCAATGCTATGCTATTCACGGAAGAA 308
22 nhlsTTPAsnArgLeuAArgAspAspAlaAlaAsnLeuLysSerLysGlyI 39
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
309 TCTTGGTTACATGCGTGTATTAAGCAAAAGAACTGCGATCGATGGGGA 358
39 leThraAlaValTTPrhLeuProAlaTTPrhLysGlyLys...SerGlnAsn 54
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
359 TTACCCATTTTGGCTCCACCGGCTTATTAAGTCAAGCTTTGGCACAGAG 408
55 AspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyLysPheAsn 70
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
409 GAGCCCGGTTATGCTGTATATGACCTGTACGATCTGGGGAATTTCAT 456
seq_name: gb_est1:AW709933

```

seq\_documentation\_block: 436 bp mRNA EST 25-APR-2000  
 LOCUS AW709933 d9b06ne.f1 Neurospora crassa evening cDNA library Neurospora crassa  
 DEFINITION d9b06ne.f1 Neurospora crassa evening cDNA library Neurospora crassa  
 CDNA clone d9b06ne 5', mRNA sequence.  
 ACCESSION AW709933  
 VERSION AW709933.1 GI:7599010  
 KEYWORDS EST.  
 SOURCE Neurospora crassa.  
 ORGANISM Neurospora crassa.  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Sordariales; Sordariaceae; Neurospora.  
 1 (bases 1 to 436)  
 AUTHORs Zhu, H., Lai, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.  
 TITLE Two Neurospora crassa EST databases  
 JOURNAL Unpublished (1998)  
 COMMENT Other\_ESTs: d9b06ne.r1  
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu  
 Department of Chemistry and Biochemistry  
 Advanced Center for Genome Technology, University of Oklahoma  
 620 Parrington Oval, Norman, OK 73019, USA  
 Tel: 405 325 4912  
 Fax: 405 325 7762  
 Email: broe@ou.edu  
 We anticipate the future release of the cDNA clones to the Fungal  
 Genetics Stock Center  
 Seq primer: Universal Forward Primer  
 High quality sequence stop: 424.  
 Location/Qualifiers

FEATURES  
 source 1..436  
 /organism="Neurospora crassa"  
 /strain="Strain 30-7 (bd; A)"  
 /db\_xref="taxon:5141"  
 /clone="d9b06ne"  
 /clone\_id="Neurospora crassa evening cDNA library"  
 /tissue\_type="tissue harvested following 22hr growth in  
 dark"  
 /note="Vector: pBluescript SK-; Site\_1: XbaI; Site\_2:  
 EcoRI; See: Bell-Perdersen, D., et al. PNAS 93:13096, 1996.  
 5' end of cDNA cloned into XbaI site of pBluescript; 3'  
 end of cDNA cloned into EcoRI site of pBluescript"

BASE COUNT 82 a 159 c 93 g 102 t  
 ORIGIN

alignment\_scores: Quality: 169.00 Length: 145  
 Ratio: 2.036 Gaps: 4  
 Percent Similarity: 57.241 Percent Identity: 31.034

alignment\_block:  
 US-09-590-375-2 x AW709933 ..

Align seg 1/1 to: AW709933 from: 1 to: 436

243 TyISerTyrThrArgAspTrpLeuThHisVal.....At 254  
 |||||.....  
 2 TACTCTTTGTCGCGAATTTCTAGCCACATCGACCGCCACGTCGCTCC 51  
 254 gAsnThrThgllyPro.....MetPheAlaValAlaGluPheTrpL 269  
 :::: |||||  
 52 TGGACCCCTGGAGCCAGGAGCGTGTTCATCGTGGCGCAATATCGGC 101  
 269 ySAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerTrpAsn 285  
 :::: |||||  
 102 GCGAAGATTCGAGTTCTCGCGGTACATCGAATTTATGACACCGC 151  
 286 HisSerValPheAspValProLeuHisTyrAsnLeu..... 297  
 |||||.....  
 152 TTGTCTCTCTCGACGTCAATTAAGTCTCAACTTCTCCGCATCTCTT 201  
 298 .....TyrAsnAlaSerAsnSerGlyGly..... 305  
 :::: |||||  
 202 AGCTTCGACACACCTCCAAAGCCTCTCCACCGGTGAGTGCTGCTC 251

306 .....TyrPheAspMetArgAsnIleLeuAsn 314  
 |||||.....  
 252 CCGGATACGATGACGCGACCGCCGACACCGACCTCCGCACTTATTCGAC 301  
 315 GlySerValValGlnLysHisProIleHisAlaValThrPheValAspAs 331  
 :::: |||||  
 302 GACACCTCTGCATCTGGAACCGCACACGCGGCTCTTGTCTGCTTAA 351  
 331 nHisAspSerGlnProGlyGluAlaLeuGluSerPheValGlnSerTrp 348  
 |||||.....  
 352 CCACGACACACAAAGGCCAATCGCTCGAAACGCCCATAGGCCCTTCT 401  
 348 helysProLeuAlaTyrAlaLeuIleLeuThrArg 359  
 |||||.....  
 402 TCATGCCCTCGCCTATTCGCTCATCTTACTTCTGC 436

QY 6 NCTMAYEFEMHLPNDGNHNNRLDDAANKSKITAVWIPAMKGTSONDVGAYADLYD 65  
 DB 33 NCTLMQYEFEMWYRPNQGNHKKRLQNDASVLAHEGITAIVWIPAKGTSONDVGAYADLYD 92  
 QY 66 LGEFNOKGTVPKRYGTGTSOLOCAGVTSKNNNGIQVYGVYVMMHKGADGTEVNAVEVNS 125  
 DB 93 LGEFNOKGTVPKRYGTGTSOLOCAGVTSKNNNGIQVYGVYVMMHKGADGTEVNAVEVNS 152  
 QY 126 NNNOESGTEYTAEMTKEDPEGRGNTSHNEKRWYHFGDTMDOSROJNKTYKRGCK 185  
 DB 153 DNKNVYSGHRIKAWTHFHPGRGSTYSDFKMWHYHFGDTMDOSROJNKTYKRGCK 209  
 QY 186 AMDWEVDIENGNYDYLMATADIDMPEVYNELRNNGVMTNTNLNDFGRIDAVKIKKSY 245  
 DB 210 AMDWEVSNNGNYDYLMATADIDMPEVYNELRNNGVMTNTNLNDFGRIDAVKIKKSY 269  
 QY 246 TRDMITVHANTGTGKPMFAVEKMDLAIENYLNKTSNNHSEVDFVPLHYNLNANSNG 305  
 DB 270 LRDVNNHVEKTKEMFVYAEVQMDGLAENYLNKTSNNHSEVDFVPLHYNFAASTOGG 329  
 QY 306 YEDMNNIUNGVSVOKHPIHATFVNNDHSDGSEALESPVQSFKEPLAYALLITREOGYPS 365  
 DB 330 GIDMKRLKSLVSKHPLAATFVDNHDHDPQSGSESTVQTFKPLAATFLLITREOGYPS 389  
 QY 366 VYGYGYGIPTHG-----VPSMKSKIDPPLAAROTVAYGTOHDYDHDHDIIGMTEGSPS 420  
 DB 390 VYGYGYGIPTHG-----VPSMKSKIDPPLAAROTVAYGTOHDYDHDHDIIGMTEGSPS 447  
 QY 421 HENSGLATIISDQSGCKNMWYVKKHAKAGVMDITGNNSGTVTINADGNGFTVNGAVS 480  
 DB 448 VANSGLAALITDTPGCAKRMVYGRONAGETWHDITGNRSEPVYINSEGEFHVNGSVS 507  
 QY 481 VAWK 485  
 DB 508 IYVOR 512

RESULT 3  
 AC P06279; 045519; STANDARD; PRT: 549 AA.  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN  
 GLUCANOHYDROLASE).  
 GN AMYS.  
 OS Bacillus stearothermophilus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Geobacillus.  
 OX NCBI\_TaxID=1422;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.  
 RX MEDLINE=85234394; PubMed=3924897;  
 RA Nakajima R., Imanaka T., Alba S.;  
 RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase  
 gene.";  
 RT J. Bacteriol. 163:401-406(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC STRAIN=DY5/PH1300;  
 RX MEDLINE=86008166; PubMed=3876333;  
 RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Uda S.;  
 RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:  
 RT homology between prokaryotic and eukaryotic alpha-amylases at the  
 RT active sites.";  
 RT J. Biochem. 96:95-103(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NZ-3;  
 RX MEDLINE=86195857; PubMed=3009417;  
 RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,  
 RA Carmona C., Requardt C.;

RT "Structural genes encoding the thermophilic alpha-amylases of  
 RT Bacillus stearothermophilus and Bacillus licheniformis.";  
 RL J. Bacteriol. 166:635-643(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P.;  
 RT "Expression of Bacillus stearothermophilus: cloning,  
 RT repression, and secretion by Escherichia coli.";  
 RL (In) Chaloupka J., Krumphanz V. (eds.);  
 RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,  
 RL New York (1987).  
 RN [5]  
 RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.  
 RC STRAIN=DY-5;  
 RX MEDLINE=86059211; PubMed=2999073;  
 RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,  
 RA Idota Y., Yamagata H., Uda S.;  
 RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by  
 RT protein-producing Bacillus brevis 47 carrying the Bacillus  
 RT stearothermophilus amylase gene.";  
 RL J. Bacteriol. 164:1182-1187(1985).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC  
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL, M11450; AAA22235.2; -;  
 DR EMBL, X02769; CAA26547.1; -;  
 DR EMBL, M57457; CAA22227.1; -;  
 DR EMBL, M13255; AAA22241.1; -;  
 DR PIR, A00845; ALBSF.  
 DR PIR, A24549; A24549.  
 DR HSSP, P06278; 1BPL.  
 DR InterPro, IPR000461; Alpha-amylase.  
 DR Pfam, PF00128; alpha-amylase; 1.  
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Signal.  
 FT SIGNAL 1 34  
 FT CHAIN 35 549  
 FT ACT\_SITE 268 268 BY SIMILARITY.  
 FT ACT\_SITE 272 272 BY SIMILARITY.  
 FT ACT\_SITE 365 365 BY SIMILARITY.  
 FT CONFLICT 13 13 M -> V (IN REF. 3).  
 FT CONFLICT 19 19 L -> W (IN REF. 3).  
 FT CONFLICT 23 23 L -> S (IN REF. 2 AND 3).  
 FT CONFLICT 31 31 A -> T (IN REF. 2 AND 3).  
 FT CONFLICT 107 107 T -> I (IN REF. 4).  
 FT CONFLICT 167 167 P -> N (IN REF. 3).  
 FT CONFLICT 179 179 S -> N (IN REF. 2, 3 AND 4).  
 FT CONFLICT 251 251 SNI -> RTN (IN REF. 4).  
 FT CONFLICT 260 262 D -> Y (IN REF. 2, 3 AND 4).  
 FT CONFLICT 284 284 M -> T (IN REF. 2 AND 3).  
 FT CONFLICT 312 312 T -> A (IN REF. 2 AND 3).  
 FT CONFLICT 338 338 R -> S (IN REF. 3).  
 FT CONFLICT 342 342 T -> N (IN REF. 3).  
 FT CONFLICT 346 346 V -> C (IN REF. 2 AND 3).  
 FT CONFLICT 376 376 WS -> R (IN REF. 2).  
 FT CONFLICT 526 527 S -> P (IN REF. 2).  
 FT CONFLICT 527 527 D -> G (IN REF. 2 AND 3).  
 FT CONFLICT 535 535 3A2D93A955E79D3 CRC64;  
 SQ SEQUENCE 549 AA; 62670 MM; 3A2D93A955E79D3 CRC64;  
 Query Match 69.8%; Score 1894.5; Dbl:1; Length 549;  
 Best Local Similarity 68.4%; Pred. No. 6.3e-122;  
 Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2001, 17:03:57 ; Search time 18.04 Seconds

(without alignments)  
965.723 Million cell updates/sec

Title: US-09-590-375-2  
Perfect score: 2713  
Sequence: 1 HHNGTNGTMMQYFEMHLPND.....ADGNGFTVNGAVSWVKQ 485

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2410	88.8	518	1 AMT6_BACS7	P19571 bacillus sp
2	1906	70.3	512	1 AMT_BACLT	P06278 bacillus li
3	1894.5	69.8	549	1 AMT_BACST	P06279 bacillus st
4	1843	67.9	514	1 AMT_BACAM	P00692 bacillus am
5	1053	38.8	494	1 AMY2_SALTY	P26613 salmonella
6	1022	37.7	495	1 AMY2_ECOLI	P26612 escherichia
7	315	11.6	1196	1 AMYB_PABPO	P21543 paenibacilli
8	294	10.8	440	1 AM3A_ORYSA	P27932 oryza sativ
9	287.5	10.6	421	1 AMYA_VIGNO	P17859 vigna mungo
10	284.5	10.5	548	1 AMT4_PSEST	P13507 pseudomonas
11	283.5	10.4	551	1 AMT4_PSESA	P22963 pseudomonas
12	281	10.4	713	1 AMYR_BACS8	P17692 bacillus sp
13	277	10.2	713	1 CDBT_BACS0	P06618 bacillus sp
14	275	10.1	712	1 CDBT_BACS3	P09121 bacillus sp
15	274.5	10.1	718	1 CDBT_BACCI	P30920 bacillus ci
16	271	10.0	713	1 CDBT_BACCI	P43379 bacillus ci
17	270	10.0	713	1 CDBT_BACSP	P30921 bacillus sp
18	269.5	9.9	718	1 CDBT_BACSP	P31747 bacillus sp
19	266.5	9.8	435	1 AM3D_ORYSA	P27933 oryza sativ
20	265	9.8	438	1 AM3B_ORYSA	P27937 oryza sativ
21	264	9.7	437	1 AM3C_ORYSA	P27939 oryza sativ
22	263.5	9.7	427	1 AMY2_HORVU	P04063 hordeum vul
23	261.5	9.6	710	1 CDBT_THETU	P26827 thermoaer
24	261	9.6	429	1 AMY6_HORVU	P04750 hordeum vul
25	260.5	9.6	428	1 AMY1_ORYSA	P17654 oryza sativ
26	260	9.6	368	1 AMY3_HORVU	P04747 hordeum vul
27	260	9.6	528	1 AMY_BACCI	P08137 bacillus ci
28	259.5	9.6	438	1 AMY1_HORVU	P00693 hordeum vul
29	255.5	9.4	718	1 CDBT_BACLI	P14014 bacillus li
30	253	9.3	703	1 CDBT_BACS2	P31746 bacillus sp
31	249.5	9.2	413	1 AMY3_WHEAT	P08117 triticum ae
32	247.5	9.1	711	1 CDBT_BACST	P31797 bacillus st
33	246	9.1	437	1 AM3E_ORYSA	P27934 oryza sativ

34	243	9.0	713	1 CDG2_PAEWA	P31835 paenibacilli
35	237.5	8.8	498	1 AMYA_ASPAW	P002905 aspergillus
36	237.5	8.8	499	1 AMYB_ASPAW	P002906 aspergillus
37	236.5	8.7	443	1 AM2A_ORYSA	P27935 oryza sativ
38	233.5	8.6	499	1 AMYA_ASPOR	P10529 aspergillus
39	232.5	8.6	445	1 AMY2_ORYSA	P27941 oryza sativ
40	231	8.5	717	1 AMYM_BACST	P19531 bacillus st
41	230.5	8.5	499	1 AMY_ASPSH	P30292 aspergillus
42	225	8.3	714	1 CDG1_PAEWA	P04830 paenibacilli
43	223.5	8.2	441	1 MGT_A_THERA	P80099 thermotoga
44	222	8.2	442	1 MGT_A_THERA	P08956 thermotoga
45	219	8.1	494	1 AMY1_SACPI	P21567 saccharomyce

## ALIGNMENTS

RESULT ID	1	AMT6_BACS7	STANDARD:	PRT:	518 AA.
AC	P19571:				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE PRECURSOR (EC 3.2.1.98) (66-AMYLASE)				
DE	(MALTOHEXAOSIDE-PRODUCING AMYLASE) (EXO-MALTOHEXAOMYDROLASE).				
OS	Bacillus sp. (strain 707).				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;				
OX	Bacillus/Staphylococcus group; Bacillus.				
NCBI_TaxID=1416;					
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.				
RX	MEDLINE=88162814; PubMed=3258152.				
RA	Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;				
RT	Nucleotide sequence of the maltotetraose-producing amylase gene from				
RT	an alkaliphilic Bacillus sp. #707 and structural similarity to				
RL	liquefying type alpha-amylases.";				
RL	Biochem. Biophys. Res. Commun. 151:25-31(1988).				
CC	-I- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC LINKAGES				
CC	IN AMYLACROUS POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE				
CC	MALTOHEXAOSIDE RESIDUES FROM THE NON-REDUCING CHAIN ENDS.				
CC	-I- PATHWAY: DEGRADATION OF STARCH.				
CC	-I- SUBCELLULAR LOCATION: SECRETED.				
CC	-I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO				
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL; M18862; AAA2231.1; -				
DR	PIR; A27705; A27705.				
DR	HSSP; P06278; 1BPL.				
DR	InterPro; IPR000461; Alpha.amylase.				
DR	PIfam; PF00128; alpha-amylase; 1.				
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.				
FT	SIGNAL				
FT	CHAIN				
SO	SEQUENCE				

Query Match 88.8%; Score 2410; DB 1; Length 518;  
Best Local Similarity 86.4%; Pred. No. 4.7e-157;  
Matches 419; Conservative 36; Mismatches 30; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEMHLPNDGHHMNRLLRDDANIKSGITAVIPAMKGTSONDVGCA 60  
DB 34 HHNGTNGTMMQYFEMHLPNDGHHMNRLLNSDASLKSIGITAVIPAMKGTSONDVGCA 93

OY 61 YDIYDLGEFNQKGVTRTKYSTRSOLQCAVTSKNNCIQYGGVYVNMHKGAGDTEWNAV 120  
 |||||  
 DB 94 YDIYDLGEFNQKGVTRTKYSTRSOLQCAVTSKNNCIQYGGVYVNMHKGAGDTEWNAV 153  
 |||||  
 OY 121 EVNRSNNQGEISGVYTEAVTKFDFPGRGNTSHNFKRWYHFDGTDMDOSROLQNKYKE 180  
 |||||  
 DB 154 EVNRSNNQGEISGVYTEAVTKFDFPGRGNTSHNFKRWYHFDGTDMDOSROLQNKYKE 213  
 |||||  
 OY 181 RGTGKAMDWEVDLENGVYDYLMTADIDMDHPEYINELRNKGVYTTNLNIGRIDAVKH 240  
 |||||  
 DB 214 RGHKAMDWEVDLENGVYDYLMTADIDMDHPEYINELRNKGVYTTNLNIGRIDAVKH 273  
 |||||  
 OY 241 IKYSTRTDLTHVNTGKRPMEFAVEFMKNDLAIENYLNKTSNHSVDFVPLHYNLNA 300  
 |||||  
 DB 274 IKYSTRTDLTHVNTGKRPMEFAVEFMKNDLAIENYLNKTSNHSVDFVPLHYNLNA 333  
 |||||  
 OY 301 SNSGCFPMRNLINGSVYOKHPIHAYTFVDNHDSPGEALSEFVSQFPLAVALITRE 360  
 |||||  
 DB 334 SKSGNMYMRNIFNCTVYGRHPSHAVTFVDNHDSPGEALSEFVSQFPLAVALITRE 393  
 |||||  
 OY 361 OGYSVFYGDYIGPTHEVPSMKSDIPLAQRQYVAGTQHDYFHHDIIGWTRGDS 420  
 |||||  
 DB 394 OGYSVFYGDYIGPTHEVPSMKSDIPLAQRQYVAGTQHDYFHHDIIGWTRGDS 453  
 |||||  
 OY 421 HNSGCIATMSDGPNGNMYVYGHKAGQVWRDITGNSGTVTINADGNGFTVNGGAYS 480  
 |||||  
 DB 454 HNSGCIATMSDGPNGNMYVYGHKAGQVWRDITGNSGTVTINADGNGFTVNGGAYS 513  
 |||||  
 OY 481 VVWKQ 485  
 |||||  
 DB 514 IWNK 518  
 |||||

RESULT 2  
 AMT\_BACLI STANDARD: PRT: 512 AA.

AC P06278;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN  
 DE GLUCANOHYDROLASE).  
 GN AMYS OR AMYL.  
 OS Bacillus licheniformis.  
 OS Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OC NCBI\_TaxID=1402;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RC SMRAIN-ATCC 27811;  
 RC MEDLINE-6611694; PubMed-2418011;  
 RA YUKI T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,  
 RA Tsukagoshi N., Uda K.,  
 RA "Complete nucleotide sequence of a gene coding for heat- and  
 RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the  
 RT amino acid sequences of three bacterial liquefying alpha-amylases  
 RT deduced from the DNA sequences.";  
 RL J. Biochem. 98:1147-1156(1985).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE-86135857; PubMed-3009417;  
 RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,  
 RA Carmona C., Reguad C.,  
 RT "Structural genes encoding the thermophilic alpha-amylases of  
 RT Bacillus stearothermophilus and Bacillus licheniformis.";  
 RL J. Bacteriol. 166:635-643(1986).  
 [3]  
 RP SEQUENCE OF 1-104 FROM N.A.  
 RP MEDLINE-84185455; PubMed-6609154;  
 RA Stephens M.A., Orlepp S.A., Ollington J.F., McConnell D.J.,  
 RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis  
 P alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";  
 P Bacteriol. 158:369-372(1984).

RN [4]  
 RP SEQUENCE OF 1-29 FROM N.A.  
 RX MEDLINE-89213924; PubMed-2540150;  
 RA Lacle B.M., Chambliss G.H., McConnell D.J.,  
 RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to  
 RT promoter-independent catalytic repression in Bacillus subtilis.";  
 RL J. Bacteriol. 171:2435-2442(1989).  
 [5]  
 RP SEQUENCE OF 30-47.  
 RX MEDLINE-82098050; PubMed-6172418;  
 RA Kuhn H., Fietzek P.P., Lampen J.O.,  
 RT "N-terminal amino acid sequence of Bacillus licheniformis  
 RT alpha-amylase: comparison with Bacillus amyloliquefaciens and  
 RT Bacillus subtilis enzymes.";  
 RL J. Bacteriol. 149:372-373(1982).  
 [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RC STRAIN-ATCC 27811;  
 RX MEDLINE-95182462; PubMed-7877175;  
 RA Machius M., Wiegand G., Huber R.,  
 RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-  
 RT amylase at 2.2-A resolution.";  
 RL J. Mol. Biol. 246:545-559(1995).  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSTS OF 1,4-ALPHA-GLUCOSIDIC  
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
 CC -1- BIOTECHNOLOGY: USED IN THE FOOD INDUSTRY FOR HIGH TEMPERATURE  
 CC LIOUEFACTION OF STARCH-CONTAINING MASHES AND IN THE DETERGENT  
 CC INDUSTRY TO REMOVE STARCH. SOLD UNDER THE NAME TERAMYL BY  
 CC NOVOZYMES.  
 CC -1- MISCELLANEOUS: ABLE TO WORK AT RELATIVELY HIGH (ALKALINE) PH  
 CC VALUES (UP TO PH 11) AND AT HIGH TEMPERATURES (UP TO 100 DEGREE  
 CC CELSIUS).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-slb.ch/announce/>  
 CC or send an email to [license@isb-slb.ch](mailto:license@isb-slb.ch)).  
 CC -----  
 DR EMBL: X03236; CAA26981.1; -  
 DR EMBL: M38570; AAA22226.1; -  
 DR EMBL: M13256; AAA22240.1; -  
 DR EMBL: K01984; AAA22193.1; -  
 DR EMBL: M26412; AAA22237.1; -  
 DR EMBL: A17930; CAA01355.1; -  
 DR PIR: A00844; ALBSL.  
 DR PIR: B24549; -  
 DR PIR: A26151; A26151.  
 DR PDB: 1BPL; 17-AUG-96.  
 DR PDB: 1VJS; 12-MAR-97.  
 DR InterPro: IPR000461; Alpha-amylase.  
 DR Pfam: PF00128; alpha-amylase; 1.  
 KW Hydroxylase; Glycosidase; Carbohydrate metabolism; Signal; 3D-structure.  
 FT SIGNAL 1 29  
 FT CHAIN 30 512  
 FT ACT\_SITE 260 260  
 FT ACT\_SITE 264 264  
 FT ACT\_SITE 357 357  
 FT CONFLICT 38 38  
 FT CONFLICT 163 163  
 FT CONFLICT 339 339  
 FT CONFLICT 349 349  
 FT SEQUENCE 512 AA; 58549 MW; D8BB7759CD4C482 CRC64;  
 Query Match 70.3%; Score 1906; DB 1; Length 512;  
 Best Local Similarity 69.1%; Pred. No. 9,6e-123;  
 Matches 335; Conservative 67; Mismatches 73; Indels 10; Gaps 4;

Db 447 DSSAAKGLAALITDGGSKRMRYAGLKNAGETWYDITGNRSDFVTKIGSDGNGEFVNDG 506  
 QY 478 AVSVVVKQ 485  
 Db 507 SVSYVQK 514

## RESULT 5

AMV2\_SALTY  
 ID AMV2\_SALTY STANDARD; PRT; 494 AA.  
 AC P26613;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE CYTOPLASMIC ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN  
 DE GLUCANOHYDROLASE).  
 GN AMYA.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OC NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JW1103;  
 RX MEDLINE=93015717; PubMed=1400215;  
 RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;  
 RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA";  
 RL J. Bacteriol. 174:6644-6652(1992).  
 RN [2]  
 RP SEQUENCE OF 1-6 FROM N.A.  
 RC STRAIN=JW1103;  
 RX MEDLINE=92407478; PubMed=1527488;  
 RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;  
 RT "Subdivision of flagellar region III of the Escherichia coli and  
 RT Salmonella typhimurium chromosomes and identification of two  
 RT additional flagellar genes";  
 RL J. Gen. Microbiol. 138:1051-1065(1992).  
 RN [3]  
 RP SEQUENCE OF 476-494 FROM N.A.  
 RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;  
 RL Submitted (MAR-1993) to the EMBL/Genbank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC  
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L01643; AAA27110.1; -;  
 DR EMBL; M85241; AAA27079.1; -;  
 DR EMBL; L13280; AAA71970.1; -;  
 DR PIR; B45738; B45738.  
 DR HSP; P06278; IBPL.  
 DR StyGene; SG10011; amyA.  
 DR InterPro; IPR000461; Alpha\_amylase.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 KW Hydrolase; Glycosidase; Carbohydrate metabolism.  
 FT ACT\_SITE 235 235 BY SIMILARITY.  
 FT ACT\_SITE 239 239 BY SIMILARITY.  
 FT ACT\_SITE 332 332 BY SIMILARITY.  
 SQ SEQUENCE 494 AA; 56496 MW; 4FA6BDBFEDD5E47C CRC64;

Query Match

38.8%; Score 1053; DB 1; Length 494;

Best Local Similarity

42.1%; Pred. No. 1;le-64;

Matches 207; Conservative 84; Mismatches 183; Indels 18; Gaps 6;  
 QY 6 NCTMMQYFEWHLPLNDGNHNRRLRDDAANLAKSKGITAWIPPAWKGTSQN-DVYGAGVDLY 64  
 Db 3 NPTLLQYFHWYYPDGGKLSWELAEADGLNDIGINMYWLPACKGASGGYSGVGYDYDLF 62  
 QY 65 DLGEFNQKGTVRTKYGRSLOQGAVTSLKNNGIOYGVVNNHKGADGTEMVNAVEVNR 124  
 Db 63 DLGEFDQKGTIATKYGDKRQLLTALDAKKNNIAVLDDVVVNNHKGADKEXIRVQRVQ 122  
 QY 125 SNRQEIISGEYTIETAWTKFDFFPGRNTHSNFKRWYHFDGTDWDSQROLQNIYKFRG-- 182  
 Db 123 DDRQTIDDNIIIECEGWTRYTFPARAGQYSNFIWYHCFSGIDHTENPD-EDGIFKIVNDY 181  
 QY 183 TGKADWEVDIENGNDYLMYADIDMDHPEVINELRWGVVYNTNLNLDGFRIDAVKHK 242  
 Db 182 TGDGNDQVDDMGNFYLMGENIDFRNHAVTEIKYARWVMEQTHCDGFRLDVAVKHIP 241  
 QY 243 YSYTRDMLTHVRNTTKPMFAVEFWKNDLAAIENYLNKTSWNHSDVDPVLYLYNASN 302  
 Db 242 AWFYKEWIEHVQAVAPKPLFTVAEYWSHEVDKLTQYIDQVKGKTLMDAPLQMKFHEASR 301  
 QY 303 SGGYFDMRNILNGSVQOKHPIHVTVDNHDSDQCEALESFVQSWFKPLAYALILTREG 362  
 Db 302 QGAEDMRHIFTGLVEADPFHVTLVANHDTPQLQALEAPVEPWFKPLAYALILLRENG 361  
 QY 363 YPSVYFGDYGCIPTH-----GVPSMKSKIDPLLOAROTYAYGTQHDYFDHDI 411  
 Db 362 VPSVYFDLYGASYEDSGENETCRVDMPTV-NOLDRLILARQFAHGIGTFLFFHPNCI 420  
 QY 412 GWTREGDSHPSNGLATIMSDPGGKNWYVGHKHAQGVWRDITGNRSQVTVINADGWN 471  
 Db 421 AFSRSGTEENP-CCVVVLSNGDDGKTLGLGDNVANKTWDRDFSSNRDEYVVTNDQGEAT 478  
 QY 472 PTVNGAVSVWV 483  
 Db 479 FFCNAGSVSVWV 490  
 RESULT 6  
 AMV2\_ECOLI  
 ID AMV2\_ECOLI STANDARD; PRT; 495 AA.  
 AC P26612; P78072;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CYTOPLASMIC ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN  
 DE GLUCANOHYDROLASE).  
 GN AMYA OR B1927.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OC NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JA11;  
 RX MEDLINE=93015717; PubMed=1400215;  
 RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;  
 RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA";  
 RL J. Bacteriol. 174:6644-6652(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12";  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;

[illegible]

		Query Match	37.7%;	Score 1022;	DB 1:	Length 495;
		Best Local Similarity	41.1%;	Pred No. 1 4e-2;		
		Matches 202;	Conservative 82;	Mismatches 191;	Indels 16;	Gaps
Qy	6	NGTMMQTFEHLPLNDGNHNRRLDDAANKSKGITAVTWTPPAWKGTSON-DYVGAGAYDLY	64			
Ddb	3	NPTLLQCFHWYIPGGKLMFLAEARDFGNDIGINMVLPPPAYKGASGGYSVGYDSYDLF	62			
Qy	65	DLGFENQKGTVRTKYGRSLQSGAVTSLKNNGIQTVDVVNHHKGDGATGMVNVEVNR	124			



\*Structural and functional roles of cysteine residues of Bacillus polymyxa beta-amylase.\*;  
 Biochemistry 30:4594-4599(1991).  
 CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLITICALLY CLEAVED TO PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDA ALPHA-AMYLASE AFTER SECRETION.  
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE MALTOSE UNITS FROM THE NON-REDUCING ENDS OF THE CHAINS.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
 CC -1- SUBCELLULAR LOCATION: SECRETED.  
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO FAMILY 14 OF GLYCOSYL HYDROLASES (BETA-AMYLASES).  
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M15817; AAA85446.1; -;  
 DR EMBL; Y00150; CAA68344.1; -;  
 DR PIR; A29130; A29130.  
 DR PIR; A29108; A29108.  
 DR PIR; A32251; A32251.  
 DR HSP; P43379; ITCM.  
 DR InterPro; IPR000461; Alpha\_amylase.  
 DR InterPro; IPR001554; Glyco\_hydro\_14.  
 DR Pfam; PF00128; alpha-amylase; 1.  
 DR Pfam; PF01373; Glyco\_hydro\_14; 1.  
 DR PRINTS; PR00750; BETAAMYLASE.  
 DR PRINTS; PR00841; GUHYDLASE1A.  
 DR PROSITE; PS00506; BETA\_AMYLASE\_1; 1.  
 DR PROSITE; PS00679; BETA\_AMYLASE\_2; 1.  
 KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;  
 KW Polysaccharide degradation; Repeat.  
 FT SIGNAL 1 35  
 FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.  
 FT DOMAIN 36 454 BETA-AMYLASE.  
 FT REPEAT 455 558  
 FT REPEAT 565 668  
 FT DOMAIN 669 1196  
 FT DSULEFID 118 126  
 FT ACT\_SITE 124 124  
 FT ACT\_SITE 198 198  
 FT MUTAGEN 118 118  
 FT MUTAGEN 126 126  
 FT MUTAGEN 358 358  
 FT CONFLICT 1 1  
 FT CONFLICT 67 67  
 FT CONFLICT 100 100  
 FT CONFLICT 154 154  
 FT CONFLICT 177 177  
 FT CONFLICT 227 228  
 FT CONFLICT 330 330  
 FT CONFLICT 425 425  
 FT CONFLICT 493 493  
 FT CONFLICT 532 532  
 FT CONFLICT 559 559  
 FT CONFLICT 665 665  
 FT CONFLICT 681 681  
 FT CONFLICT 686 686  
 FT CONFLICT 725 728  
 FT CONFLICT 736 736  
 FT CONFLICT 741 741  
 FT CONFLICT 758 758  
 FT CONFLICT 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;  
 SO SEQUENCE

Query Match 11.6%; Score 315; DB 1; Length 1196;  
 Best Local Similarity 24.1%; Pred. No. 5 5e-14;  
 Matches 125; Conservative 67; Mismatches 189; Indels 138; Gaps 25;  
 QY 1 HHNCTGTMQYFEWHLPNDGNHNRRLDDAANLKSGITAVWIPPAWKGTQNDV-GYG 59  
 DB 766 NYGFGNSNSDQRKWH-----GGDFQGLINKLDYIKNMGTAIWITPTVMQKSEYAHGYH 821  
 QY 60 AYDLYDLGEFNOKGTVTKYKTRSQLOGAVTSLKNNGIOYGVYVMNHKKGADGETWVNA 119  
 DB 822 TYDFY-----AVDGHGLTMDKQLQELVRKAHDKKIAVMVYVVAHTG----- 862  
 QY 120 VEVNRNRNQEISGEYIEAWTKFDF-PGRGNTHSNF-KWRVHYFDG--TDWDQSRQLQN 175  
 DB 863 -----DFQPGNGFAKAPDKADWYHHNGDITDGDYNSNQ- 897  
 QY 176 KIYFRGTGKAWDEVDIENGNYDLYMADIOMDHPVINELRNMGVYVYTNLNLGDFRI 235  
 DB 898 -----WK--IENG--DVAGLDLNLHENPATANELKNWIKWLLNETGIDGLRL 940  
 QY 236 DAVKHIKYSYTRDHLTHVRNTTGKPMFAVAFAEFKNDLAAIENYLNKTSWNHSHVDFVPLHY 295  
 DB 941 DTVKHVPKGLKDF-DQAANT-----FTMGEIFHGDPAIYVGDY---TRYLDAALDFPMY 991  
 QY 296 NLYNASNSGGYFDMNRLNGSVQKHPIHVT---FVDNHD-----SOPGEALESF 343  
 DB 992 TIKDV--FGHDSMRKIKDRYSDDRYRDAGTNGVFDNHDVKKFLNDASGKPGANYDKW 1049  
 QY 344 VQSWFKPLAYALILT-REQGYPSVYGYGYGIPHTGVPSMKSKIDPLLQARQTYAGTQH 402  
 DB 1050 PQ-----LKAALGFTLTSRGIPITTYQGTQYSGGDDPA-----NRENMFNANH 1094  
 QY 403 DYFDHDIIGTWREGSDSHPNSSLATIMSDGPGCKNKM-----YVGKHKAG-----Q 449  
 DB 1095 DLYQIAKLNIVR---NNHP-----ALQNSQREKVVDDSYFSQSKNGDEAIVFINN 1145  
 QY 450 VWRDIT---GN-----RSGTVTINADGNGFTVNGGAVSV 481  
 DB 1146 SWNSQTRTIGNFDLSNGLTRLTNLSNDSVQINGNSITV 1184  
 RESULT 8  
 AM3A\_ORYSA  
 ID AM3A\_ORYSA STANDARD; PRT; 440 AA.  
 AC P27932;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE ALPHA-AMYLASE ISOZYME 3A PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).  
 GN AMYL-2 OR AMY3A.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. JAPONICA M202; TISSUE=Etiolated leaf;  
 RX MEDLINE=91329692; PubMed=1714318;  
 RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;  
 RT "Characterization of an alpha-amylase multigene cluster in rice.";  
 RL Plant Mol. Biol. 16:579-591(1991).  
 CC -1- FUNCTION: IMPORTANT FOR BREAKDOWN OF ENDOSPERM STARCH DURING GERMINATION.  
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN EMBRYO-DERIVED CALLUS TISSUE.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONES CELLS UNDER THE CONTROL OF THE PLANT HORMONE

CC	GIBBERELIC ACID AND IN THE DEVELOPING GRAINS AT A LOW LEVEL.
CC	-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; X56336; CAA39776.1; -
DR	PIR; S14958; S14958.
DR	HSP; P04063; 1AMY.
DR	Mendel; 9689; Oryza; Amy1.2.
DR	InterPro; IPR000461; Alpha-amylase.
DR	pfam; PF00128; alpha-amylase; 1.
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal;
KW	Multigene family.
FT	SIGNAL 1 26
FT	CHAIN 27 440
FT	ACT_SITE 207 207
FT	ACT_SITE 315 315
FT	CA_BIND 119 119
FT	CA_BIND 178 178
FT	SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;
SQ	-----
Query Match	10.8%; Score 294; DB 1; Length 440;
Best Local Similarity	25.8%; Pred. No. 4.5e-13;
Matches	106; Conservative 56; Mismatches 151; Indels 98; Gaps 18;
QY	9 MMQYFEW-HLPDNGHNHNRLLRDAANLKSIGITAVWTPPAWKTSQNDYGYGAYDLYDLG 67
Db	31 LFQGFNDSWKKGQGWYMLKQDQDIASAGVTHWLPPTTHSVSQ--GYMPCRLYDLN 88
QY	68 EFNKGIVRTKYGRSOLQGAVTSLKNGIQVYGVVYMHKGGADGTEMYNAVEVNRNR 127
Db	89 -----ASKYGTGKELSLIAAFHAKGKICVADIVNHCADD----- 125
QY	128 NOEISGEYTTIEMTKFPFGRGNTHSNFKRWYHFDGTDQDQSLQNLKIKYKPRGTGKAW 187
Db	126 -KDGGRGYCI-----FKGGPRGC-----LDWGPMSICDDTQYSDGTGH-- 164
QY	188 DWEVDIENGNYDLYMYADIDMDHPEVNLNMGVYVYVNTLNLDFRIDAVKHKYSYTR 247
Db	165 -----RDTGADFAAPDIDHNLPLVQRELSDLRLRLRDVGDFGWRDLFAKGYSAVAR 218
QY	248 DMLTHVRNTTKPMFAVAEFWKNDLA-----AIENLYNKTSNHVSFV 291
Db	219 ---TVVQN--ARPSFVVAEIW-NSLSYDGDGKPAANQDQGRQELVNVKQVGGPATAFDF 272
QY	292 PLHYNLYNASNGYGFDMRNTLNG---SVQKHPIHVAFTFVDNHDSQGEALSFVSWF 348
Db	273 TTK-GILQSAVGELWNRD-KDKAPGMIGWYEPKAVTFVDNHT-----GSTQRWMP 324
QY	349 KP-----LAYALITREGYPSVFGYDYGTPTHGVPSMKSKIDPLQARQ 394
Db	325 FPSDKVLGYAVILT-HPGVPCIEFQVFDW-----NLKOEINALAATR 368
RESULT	9
ID	AMYA_VIGMU
AC	AMYA_VIGMU STANDARD; PRT; 421 AA.
DT	P17859;
DT	01-AUG-1990 (Rel. 15, Created)
DT	01-AUG-1990 (Rel. 15, Last sequence update)
DT	15-DEC-1998 (Rel. 37, Last annotation update)
DE	ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
DE	GLUCANOHYDROLASE).
GN	AMY1.1.
Q5	Vigna mungo (Rice bean) (Black gram).

OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX	NCBI_TaxID=3915;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Cotyledon;
RC	MEDLINE=90332425; PubMed=2377468;
RA	Yamauchi D., Minamikawa T.
RT	"Nucleotide sequence of cDNA for alpha-amylase from cotyledons of
RT	germinating Vigna mungo seeds.";
RL	Nucleic Acids Res. 18:4250-4250(1990).
RN	[2]
RN	SEQUENCE FROM N.A.
RN	MEDLINE=94120017; PubMed=8290640;
RA	Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT	"Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
RL	Plant Physiol. 103:1459-1459(1993)
CC	-!- CATALYTIC ACTIVITY: ENDOMYOHLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC	LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC	-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC	-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; X53049; CAA37217.1; -
DR	EMBL; X73301; CAA51734.1; -
DR	PIR; S10514; S10514.
DR	PIR; S40201; S40201.
DR	HSP; P04063; 1AMY.
DR	Mendel; 12451; VIGMU; Amy1.1.
DR	InterPro; IPR000461; Alpha-amylase.
DR	pfam; PF00128; alpha-amylase; 1
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal.
FT	SIGNAL 1 23
FT	CHAIN 24 421
FT	ACT_SITE 201 201
FT	ACT_SITE 309 309
FT	CA_BIND 113 113
FT	CA_BIND 172 172
FT	SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;
SQ	-----
Query Match	10.6%; Score 287.5; DB 1; Length 421;
Best Local Similarity	24.7%; Pred. No. 1.2e-12;
Matches	99; Conservative 48; Mismatches 137; Indels 117; Gaps 14;
QY	9 MMQYFEWHLPNCGNHNHNRLLRDAANLKSIGITAVWTPPAWKTSQNDYGYGAYDLYDLGE 68
Db	26 LFQGFNWSKKGQGWYNSLKNIPDLANAGITHVWLPPTPSQVSPE--GYLPGRLYDLN- 82
QY	69 FNQKIVRTKYGRSOLQGAVTSLKNGIQVYGVVYMHKGGADGTEMYNAVEVNRNRN 128
Db	83 -----ASKYGNELKSLIAAFHEKGIKCLADIVNH-----RTAER 119
QY	129 QEISGEYTTIEMTKFPFGRGNTHSNFKRWYHFDGTDQDQSLQNLKIKYKPRGTGKAWD 188
Db	120 KDGRIYCI-----FEG-GTPDSR-----QDWGPFICRDTAYSDGTGN--- 158
QY	189 WEVDIENGNYDLYMYADIDMDHPEVNLNMGVYVYVNTLNLDFRIDAVKHKYSYTRD 248
Db	159 -----NDSGEGYDAAPDIDHNLNPOVQRELSEWNLKTEIGFDGWRDFVKGYAPSIKI 213
QY	249 WLTHVRNTTKPMFAVAEFW-----KNDLAAIENLYNKTSNHVSFVDPVL 293
Db	214 YMEQT-----KPDFAVGEKWDISYSGDGKPNYNQDQSHRGALVNVWESAGGATAFD- 265



Db 326 QHFWALQDGLIROAVAYILT-SPGTPVYVWVSHMYDMWYGDF-----IRQLI 370  
QY 391 QARQYVANGTQHDYFDHDIIGTWREGDSHPNSGLATIMSDGPGGNKWMYV----- 442  
Db 371 QVRR--AAGVRAD-----SALSFH--SGYSLVATVSGSQTLVVALNSDLGN 414  
QY 443 -GKHKAG-----QWRDITGNRSG 460  
Db 415 PCOVASGFSSEAVNASGQVRWRSRGSGGG 446  
  
RESULT 11  
ID AMT4\_PSESA STANDARD; PRT; 551 AA.  
AC P22963;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE PRECURSOR (EC 3.2.1.60) (G4-  
DE AMYLASE) (MALTOTETRAOSE-FORMING AMYLASE) (EXO-MALTOTETRAHYDROLASE)  
DE (MALTOTETRAOSE-FORMING EXO-AMYLASE).  
GN MTA.  
OS Pseudomonas saccharophila.  
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae.  
OX NCBI\_TaxID=304;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=IAM 1504;  
RX MEDLINE=90005970; PubMed=2676600;  
RA Zhou J., Baba T., Takano T., Kobayashi S., Arai Y.;  
RA "Nucleotide sequence of the maltotetraohydrolase gene from  
RA Pseudomonas saccharophila."  
RT Pseudomonas saccharophila.  
RL FEBS Lett. 255:37-41(1989).  
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-D-GLUCOSIDIC LINKAGES  
CC IN AMYLACEOUS POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE  
CC MALTOTETRAOSE RESIDUES FROM THE NON-REDUCING CHAIN ENDS.  
CC -1- COFACTOR: BINDS TWO CALCIUM IONS (BY SIMILARITY).  
CC -1- PATHWAY: DEGRADATION OF STARCH.  
CC -1- SUBCELLULAR LOCATION: SECRETED.  
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO  
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL: X16732; CAA34708.1; -  
DR PIR: S05667; S05667.  
DR HSP: E13507; 2AMG.  
DR InterPro: IPRO00461; Alpha\_amylase.  
DR Pfam: IPRO02044; CBD\_4.  
DR Pfam: PF00128; alpha-amylase; 1.  
DR Pfam: PF00686; CBD\_4; 1.  
DR Probom: PD001568; CBD\_4; 1.  
KW Hydrolase; Glycosidase; Signal; Carbohydrate metabolism; Calcium.  
FT SIGNAL 1 21  
FT CHAIN 22 551  
FT DISULFID 161 171  
FT DISULFID 237 272  
FT CA\_BIND 22 22  
FT CA\_BIND 23 23  
FT CA\_BIND 34 34  
FT CA\_BIND 37 37  
FT CA\_BIND 38 38  
FT CA\_BIND 137 137  
FT CA\_BIND 172 172  
FT CA\_BIND 175 175  
FT CA\_BIND 183 183  
FT CA\_BIND 214 214  
FT ACT\_SITE 214

FT ACT\_SITE 240 240 BY SIMILARITY.  
FT ACT\_SITE 315 315 BY SIMILARITY.  
SQ SEQUENCE 551 AA; 59898 MW; F6D67D0BB235EA35 CRC64;  
  
Query Match 10.4%; Score 283.5; DB 1; Length 551;  
Best Local Similarity 24.8%; Pred. No. 3.le-12;  
Matches 131; Conservative 62; Mismatches 183; Indels 153; Gaps 23;  
  
QY 2 HNGTNGTMQYFEWHL-----PNDGNHNRRLRDAANLKSIGITAVWIPPAWK----- 49  
Db 33 YHGDEIILQGFHNVVREAPND--WYNILRQQAISIAADGFSAINWMPVWRDSSWTDG 90  
QY 50 GTSQNDVYGAYDLYDLGFEFNQKQVTKYGTGTSQLOGAVTSKNGNGIQYGVGVVNHKG 109  
Db 91 GKSGGEGYFWHD-----FNKNG-----RYGSDAQLRQAAGALGGAGVKVLYDVDPNH-- 138  
QY 110 GADTEMVNAVEVNRNNOEISGEYIEAWTKFDFPGRGNTHSNFKRWYHDFGTDWDQ 169  
Db 139 -----MNRGYPDKKEINLPACGGFW-RNDCADPGN-----YPNDCDDGD- 175  
QY 170 SRQLQNKIYKFRGTGKAWDWEVDIENGNYDILMYADIDMDHPEVINELRNNGVWYNTLN 229  
Db 176 -----REIG-GE-----SDLNTGHPQI-----YGMFRDELAN 201  
QY 230 L-----DGFRIQAVKHKIYSTRDLWTHVENTTCKPFAVAEFKNDLAAIE-NYLNKT 282  
Db 202 LRSGYGAGGFRDFVRGYAPERVDSDMSDSADSS-----FCVGLWKGFSEYPSWDWNTA 257  
QY 283 SWNH-----SVFDPVPLHYNLYNASNGGYFDMRNILNGSVVQKHPIHATVFDN 331  
Db 258 SWQIILKWSRAKCPVDFDFALKERMQN---GSVADWKHGLNGNPDPRMREVAVTFVDN 313  
QY 332 HDS-----QPGALESFVQSWFKPLAYLILITREGQYPSVF-----YGDYXGIPTHG 378  
Db 314 HDTGYSPGQNGQHWAQDGLIRQAYAYILT-SPGTPVYVWVSHMYDMWYGDF----- 365  
QY 379 VFSMSKSDPLLAQRTYAYGTQHDYFDHDIIGTWREGDSHP-----NSGLATIMSD 432  
Db 366 -----IRQLQVVRTAGVRADSAISFHSYSGLVATVSGSQTLVVALNSDLANPGQV 418  
QY 433 GPGGNKWMYVGVKHKAGQVWRDITGNRSQVTTINADGNGNFTVNGGAVSV 481  
Db 419 ASGSFSEAVNASGQVRWRSRG-----DGGNGDGGEGGLVNV 457  
  
RESULT 12  
ID AMYR\_BACS8  
AC P17692;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE RAW-STARCH-DIGESTING AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-  
DE GLUCAN GLUCANOHYDROLASE).  
OS Bacillus sp. (strain B1018).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1417;  
RN [1]  
RN SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.  
RX MEDLINE=90147765; PubMed=1689153;  
RA Itokor P., Tsukagoshi N., Uda S.;  
RA "Nucleotide sequence of the raw-starch-digesting amylase gene from  
RA Bacillus sp. B1018 and its strong homology to the cyclodextrin  
RA glucanotransferase genes."  
RL Biochem. Biophys. Res. Commun. 166:630-636(1990).  
CC -1- FUNCTION: THIS ENDO-TYPE ADSORBABLE AMYLASE IS CAPABLE TO  
CC DIGEST RAW-STARCH.  
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC  
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.  
CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: SECRETED.



CC	SEQUENCE	713 AA; 78340 MW; 524B259526B56C52 CRC64;	
CC	Query Match	10.1%; Score 277; DB 1; Length 713;	
CC	Best Local Similarity	22.4%; Pred. No. 1.2e-11;	
CC	Matches 114; Conservative	87; Mismatches 201; Indels 104; Gaps 23;	
QY	21 GNHW-----NLRDRAANLKS	GITAVWIPPAWKG-----TSQNDVG	GVGYDLYDLGEF 69
DB	78 GGDWQGIINKIND--GYLTGMG	ITAIWISQPVENIYSVINSGVNTAY	HGYWARDFKT 135
QY	70 NQKGYTRTKYGRSOLQ	GAVTSLKNGIOVYGDVVMNHKGGAD	GTEMVNAVVRNRRNQ 129
DB	136 N-----PAYGTMDQF	KNLIDTAHANIKVIIDFAPNHT	SPASSDD--PSFAENGRLYDNG 188
QY	130 EISGEYITIAWTKFDP	PGRGNTHSNFKRWYHFDGTDWDS	QROLQNKIKYKFGTGKADW 189
DB	189 NLGGYNTDQNLF-----	HHYGGTDFS---TIENGIYK----	NLYDL 224
QY	190 EVDIENGNDYLMYAD	IDMDHPEVINELRNMGVWYNTNL	LDGFRIDAVKHIKYSYTRDW 249
DB	225 -ADLNHN-----SSVDV	YLKDAIK--KNDLA-AIENYLNK	TSWNHSVDFVPLHYNLYNAS 269
QY	250 LTHVNTTKGPMFAV	AEFW--KNDLA-AIENYLNK	TSWNHSVDFVPLHYNLYNAS 306
DB	270 MATINNY--KPVTF	GEWFLGVNEISPEYHOFANES	MSLLDFRFAKAKARQVFRD 327
QY	307 FDMRNLINGSVQK	PIH-AVTFVDNHSQPG	EALSFVQSWFKPLAYALIL 365
DB	328 YGLKAMLEGEVDY	QVNDQVTFIDNHDMERFHT	SNDRKLEQALFTL---TSRGVFA 384
QY	366 VFYGDYGIPTHG	VPMSKMS-----KIDPLLO	ARQVYAYGTQHDYFDHHD 409
DB	385 IYTSQYMSGNDP	DNARLPSEFTTTTAYQV	IQKLAPLRKSNPALAYGST 444
QY	410 IIGWTRGDSHP	NSGLATIMSDPGGNKMYG	KHAGQV-----WFDITGN-- 460
DB	445 VIIYERKFGN--	NVAVVAI-----NRNMT	PASITGLVTSRRASYNDV 494
QY	461 TVTINADG-WG	NFTVNGGAVSVW 482	
DB	495 TLTVGAGGA	SNFTLAPGCTAVW 517	
RESULT 14	CDGT_BACS3	STANDARD; PRT; 712 AA.	
ID	CDGT_BACS3		
AC	P09121;		
DT	01-MAR-1989 (Rel. 10, Created)		
DT	01-JUL-1993 (Rel. 26, Last sequence update)		
DT	01-NOV-1995 (Rel. 32, Last annotation update)		
DE	CYCLOMALTODEXTRIN	GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)	
DE	(CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).		
GN	CGT.		
OS	Bacillus sp. (strain 38-2).		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;		
OC	Bacillus/Staphylococcus group; Bacillus.		
OX	NCBI_TaxID=1412;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.		
RX	MEDLINE=89036108; PubMed=2572812;		
RA	Kaneko T., Hamamoto T., Horikoshi K.		
RT	"Nucleotide sequence of the cyclomaltodextrin		
RT	glucanotransferase gene from the alkalophilic Bacillus sp. strain no.		
RT	38-2."		
RL	J. Gen. Microbiol. 134:97-105(1988).		
RN	[2]		
RP	SEQUENCE OF 1-586 FROM N.A.		
RA	Hamamoto T., Kaneko T., Horikoshi K.		
RT	"Nucleotide sequence of the cyclomaltodextrin glucanotransferase		
RT	(CGTase) gene from alkalophilic Bacillus sp. strain No. 38-2."		
RL	Agric. Biol. Chem. 51:2019-2022(1987).		
CC	-!- CATALYTIC ACTIVITY: DEGRADE STARCH TO CYCLODEXTRINS BY FORMATION		

CC	OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.		
CC	-!- COFACTOR: BINDS TWO CALCIUM IONS.		
CC	-!- SUBUNIT: MONOMER.		
CC	-!- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE		
CC	IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND		
CC	IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER		
CC	ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN		
CC	ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE		
CC	MALTOOLIGOSACCHARIDE PRODUCED.		
CC	-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO		
CC	KNOWN AS THE ALPHA-AMYLASE FAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/</a> ).		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .		
CC	EMBL; M19880; AAA22309.1; -		
DR	EMBL; D00129; BAA00077.1; -		
DR	PIR; S24193; ALBSG3.		
DR	HSP; P05618; 1PAM.		
DR	InterPro; IPR000461; Alpha_amylase.		
DR	InterPro; IPR002044; CBD_4.		
DR	InterPro; IPR002909; IPT_TIG.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	Pfam; PF00686; CBD_4; 1.		
DR	Pfam; PF01833; TIG; 1.		
DR	ProDom; PD001568; CBD_4; 1.		
DR	Transferase; Glycosyltransferase; Calcium; Signal.		
KW	SIGNAL		
FT	CHAIN	28 712	CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT	DOMAIN	28 165	AI.
FT	DOMAIN	166 229	B.
FT	DOMAIN	230 433	A2.
FT	DOMAIN	434 522	C.
FT	DOMAIN	523 608	D.
FT	DOMAIN	609 712	E.
FT	DISULFID	70 77	BY SIMILARITY.
FT	ACT_SITE	256 256	BY SIMILARITY.
FT	ACT_SITE	284 284	BY SIMILARITY.
FT	ACT_SITE	355 355	BY SIMILARITY.
FT	CONFLICT	582 586	VPGGI -> SWRHL (IN REF. 2).
FT	SEQUENCE	712 AA; 78249 MW; 4FAA8F70BEF818F9 CRC64;	
QY	Query Match	10.1%; Score 275; DB 1; Length 712;	
QY	Best Local Similarity	22.4%; Pred. No. 1.6e-11;	
QY	Matches 114; Conservative	90; Mismatches 190; Indels 114; Gaps 27;	
QY	21 GNHW-----NLRDRAANLKS	GITAVWIPPP-----AMKGTSON	DVGYGAVDLYDLGEFNOK 72
DB	78 GGDWQGIINKIND--GYLTGMG	ITAIWISQPVENIYSVINSGVNTAY	HGYWARDFKK- 134
QY	73 GTVRTKYGRSOLQ	GAVTSLKNGIOVYGDVVMNHKGGAD	GTEMVNAVVRNRRNOEIS 132
DB	135 --TNPAYGTMDQF	KNLIDTAHANIKVIIDFAPNHT	SPASSDD--PSFAENGRLYDNG 191
QY	133 GEYITIAWTKFDP	PGRGNTHSNFKRWYHFDGTDWDS	QROLQNKIKYKFGTGKADW 192
DB	192 GGYTNDQNLF-----	HHYGGTDFS---TIENGIYK----	NLYDL-AD 226
QY	193 IENGNDYLMYAD	IDMDHPEVINELRNMGVWYNTNL	LDGFRIDAVKHIKYSYTRDW 252
DB	227 LNHNN-----SSVDV	YLKDAIK--KNDLA-AIENYLNK	TSWNHSVDFVPLHYNLYNA-- 272
QY	253 VRNTTKGPMFAV	AEFW--KNDLA-AIENYLNK	TSWNHSVDFVPLHYNLYNA-- 307
DB	273 INNY--KPVTF	GEWFLGVNEISPEYHOFANES	MSLLDFRFAKAKARQVFRD 328
QY	308 DMRNLINGSVQK	PIH-AVTFVDNHSQPG	EALSFVQSWFKPLAYALIL 366

```
Db 329 GLKAMLEGSEVDYAQVNDQVTFIDNHDMEFHTSNGDRKLEQALFTL---TSRGVPAI 385
Oy 367 EYG-DYY-----GITHGVPS-----MKSIDPLLQARQTYAGTQHDYFDHDI 410
Db 386 YGSEQYSGGNDPDNRARISFSTTTAYQVIOKLAPRKSNAIAYGSTQERWINDV 445
Oy 411 IGWTRF-----GDSHPNS--GLATIMSDPGGKMKWYVGHKKAQGVWRDITGN 457
Db 446 IYERKFNNAVAVAINNMTPASITGLVTSLPQGS-----YNDVLGG 489
Oy 458 --RSGTVTINADG-WGNTVNGVAGVSW 482
Db 490 ILNGNTLTGAGGAASNETLAPGGTAVW 517

RESULT 15
CDGT_BACCI STANDARD; PRT; 718 AA.
AC P30920;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8;
RA Nitschke L., Heeger K., Bender H., Schulz G.E.;
RT "Molecular cloning, nucleotide sequence and expression in Escherichia
RT coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus
RT circulans strain no. 8.";
RL Appl. Microbiol. Biotechnol. 33:542-546(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-91117298; PubMed=1826034;
RA Klein C., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A
RT resolution.";
RL J. Mol. Biol. 217:737-750(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-90064533; PubMed=2531228;
RA Hofmann B.E., Bender H., Schulz G.E.;
RT "Three-dimensional structure of cyclodextrin glycosyltransferase from
RT Bacillus circulans at 3.4-A resolution.";
RL J. Mol. Biol. 209:793-800(1989).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-98226626; PubMed=9558324;
RA Schmidt A.K., Cottaz S., Driquez H., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT derivative of its main product beta-cyclodextrin.";
RL Biochemistry 37:5909-5915(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE-98409292; PubMed=9738912;
RA Parsiegla G., Schmidt A.K., Schulz G.E.;
RT "Substrate binding to a cyclodextrin glycosyltransferase and
RT mutations increasing the gamma-cyclodextrin production.";
RL Eur. J. Biochem. 255:710-717(1998).
CC -1- CATALYTIC ACTIVITY: DEGRADE STARCH TO CYCLODEXTRINS BY FORMATION
CC OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.
CC -1- COFACTOR: BINDS TWO CALCIUM IONS.

-1- SUBUNIT: MONOMER.
-1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
EMBL; X68326; CAA48401.1; -.
PIR; S23674; ALBSGC.
PDB; 1CGT; 31-JAN-94.
PDB; 1CGU; 31-JAN-94.
PDB; 3CGT; 27-MAY-98.
PDB; 4CGT; 12-AUG-98.
PDB; 5CGT; 12-AUG-98.
PDB; 6CGT; 14-OCT-98.
PDB; 7CGT; 12-AUG-98.
PDB; 8CGT; 14-OCT-98.
PDB; 9CGT; 14-OCT-98.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR002044; CBD_4.
InterPro; IPR002909; IPT_TIG.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00686; CBD_4; 1.
Pfam; PF01833; TIG; 1.
ProDom; PD001568; CBD_4; 1.
Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
KW SIGNAL
FT CHAIN 1 34 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DOMAIN 35 718 A1.
FT DOMAIN 173 236 B.
FT DOMAIN 237 440 A2.
FT DOMAIN 441 528 C.
FT DOMAIN 529 614 D.
FT DOMAIN 615 718 E.
FT DISULFID 77 84
FT ACT_SITE 258
FT ACT_SITE 291
FT ACT_SITE 362
FT TURN 40 41
FT TURN 43 44
FT TURN 47 48
FT STRAND 51 53
FT HELIX 56 59
FT TURN 71 72
FT STRAND 73 73
FT TURN 75 76
FT TURN 80 81
FT STRAND 83 83
FT HELIX 88 96
FT TURN 97 98
FT HELIX 99 103
FT TURN 104 104
FT STRAND 107 109
FT STRAND 114 116
FT STRAND 121 123
FT TURN 124 125
FT STRAND 126 128
FT TURN 131 132
FT STRAND 136 142
FT TURN 144 146
FT HELIX 149 161
FT TURN 162
```





Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2410	88.8	518	1	A27705	alpha-amylase (EC
2	1910.5	70.4	549	1	A54541	alpha-amylase (EC
3	1906	70.3	512	1	ALBSL	alpha-amylase (EC
4	1900.5	70.1	549	1	A24549	alpha-amylase (EC
5	1894.5	69.8	549	1	A24436	alpha-amylase (EC
6	1843	67.9	514	1	ALBSN	alpha-amylase (EC
7	1833	67.6	548	1	ALBSF	alpha-amylase (EC
8	1347	49.6	493	2	S15713	alpha-amylase (EC
9	1133	41.8	491	2	C86781	alpha-amylase (imp
10	1053	38.8	494	1	B45738	alpha-amylase (EC
11	1022	37.7	495	1	A45738	alpha-amylase (EC
12	1006	37.1	495	2	B85810	cytoplasmic alpha
13	393.5	14.5	217	2	A19506	alpha-amylase (EC
14	315	11.6	1196	2	A29130	beta-amylase (EC 3
15	304.5	11.2	482	2	S31478	alpha-amylase (EC
16	294	10.8	440	2	S14958	alpha-amylase (EC
17	287.5	10.6	421	2	S10514	alpha-amylase (EC
18	287	10.6	423	2	T09942	alpha-amylase (EC
19	286.5	10.6	826	2	E96720	probable alpha-am
20	283.5	10.4	551	2	S05667	glucan 1,4-alpha-m
21	281	10.4	713	2	S09196	cyclomaltodextrin
22	278	10.2	428	2	T05521	alpha-amylase (EC
23	277	10.2	713	1	ALBSG1	cyclomaltodextrin
24	275	10.1	547	2	A32803	glucan 1,4-alpha-m
25	275	10.1	712	1	ALBSG3	cyclomaltodextrin
26	274.5	10.1	718	1	ALBSG2	cyclomaltodextrin
27	271	10.0	713	2	A58800	cyclomaltodextrin
28	270	10.0	713	1	ALBSG7	cyclomaltodextrin
29	269.5	9.9	718	1	ALBSG6	cyclomaltodextrin

Db 274 IKYSTRDWINVRSGATGKNMFVAFWKNLGDIAENLYLQKTNWHSFVDPVPLHYNLYNA 333  
Qy 301 SNSGGYFDMRNILNGSVQKHPHIAVTFVDNHDSDQGEALSFVQSWFKPLAYALILTR 360  
Db 334 SKSGGNYDMRNIFNGTVQVQHPHSHAVTFVDNHDSDQGEALSFVQSWFKPLAYALILTR 393  
Qy 361 QGYPVFGDYGIPTGHGVPMSKIDPLLOARQYAYGTQHDYFDHDDIIGWTREGDSS 420  
Db 394 QGYPVFGDYGIPTGHGVPMSKIDPLLEARQYAYGTQHDYFDHDDIIGWTREGDSS 453  
Qy 421 HPSGLATITMSDGGKMWYKKGAGOVWRDITGNRSGTGTINADGWNFTVNGGAVS 480  
Db 454 HPSGLATITMSDGGKMWYKKGAGOVWRDITGNRSGTGTINADGWNFTVNGGAVS 513  
Qy 481 VVWK 485  
Db 514 IWNK 518  
RESULT 2  
A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.  
A:Reference number: A54541  
A:Accession: A54541  
A:Molecule type: DNA  
A:Residues: 1-549 <OR>  
A:Cross-references: GB:X59476  
A:Experimental source: Chromosomal DNA of strain DN1792  
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the  
C:Genetics:  
C:Start codon: GTG  
C:Function:  
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A:Pathway: glycogen/starch degradation  
C:Superfamily: alpha-amylase, amyloliquefaciens type: alpha-amylase core homology  
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-549/Product: alpha-amylase #status predicted <MAT>  
F:235-368/Domain: alpha-amylase core homology <AMY>  
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted  
F:268,298,365/Active site: Asp, Glu, Asp #status predicted  
Query Match 70.4%; Score 1910.5; DB 1; Length 549;  
Best Local Similarity 68.8%; Pred. No. 2.4e-122;  
Matches 329; Conservative 69; Mismatches 79; Indels 1; Gaps 1;  
Qy 6 NGTMMQYFEWHPNDGNHWNRLRDAANLKSGLTAVYIPPAWKGTSQNDVGYGAYDLXD 65  
Db 39 NGTMMQYFEWLPDDGLTWTVAENANLSDGITALWLPAYKGTSGDSVDGYGVYDLXD 98  
Qy 66 LGEFNQKGTVRTKYGRSLOQAGVTSKNGGIQYGVYVMNHKGAGDTEMVNAVEVNR 125  
Db 99 LGEFNQKGTVRTKYGRSLOQAGVTSKNGGIQYGVYVMNHKGAGDTEMVNAVEVNR 158  
Qy 126 NRNQEISGEYTEAWTKDFPGRGNTWNSFKRWYHFDGTWDQSRQLQNKIYKFRGTGK 185  
Db 159 DRNQEISGTQIQAWTKDFPGRGNTWNSFKRWYHFDGTWDQSRQLQNKIYKFRGTGK 217  
Qy 186 ANDWEVDIENGNYDLYMADIDMDHPEVINELRNNGWYVNTNLNLDGFRIDAVKHKYSY 245  
Db 218 ANDWEVDIENGNYDLYMADIDMDHPEVINELRNNGWYVNTNLNLDGFRIDAVKHKYSY 277  
Qy 246 TRDWLTHVTRNTGKPMFAVAFWKNLGDIAENLYLQKTNWHSFVDPVPLHYNLYNASGG 305  
Db 278 FPDWLSYVRSQTKPLFTVGEWYSYDINKLHNYITKTDGTSLSLFDAPLHNKFTASKSGG 337

Qy 306 YFDMRNILNGSVQKHPHIAVTFVDNHDSDQGEALSFVQSWFKPLAYALILTR 365  
Db 338 AFDMRTMTNTLMKQDQTLAVTFVDNHDSDQGEALSFVQSWFKPLAYALILTR 397  
Qy 366 VFYGDYGIPTGHGVPMSKIDPLLOARQYAYGTQHDYFDHDDIIGWTREGDSS 425  
Db 398 VFYGDYGIPTGHGVPMSKIDPLLOARQYAYGTQHDYFDHDDIIGWTREGDSS 457  
Qy 426 LATIMSDGPGKMWYKKGAGOVWRDITGNRSGTGTINADGWNFTVNGGAVS 483  
Db 458 LAALITDGGKMWYKKGAGOVWRDITGNRSGTGTINADGWNFTVNGGAVS 515  
RESULT 3  
ALBSL  
N:Alternates names: 1,4-alpha-D-glucan glucanohydrolase  
C:Species: Bacillus licheniformis  
C:Date: 30-Jun-1987 #sequence\_revision 24-Apr-1998 #text\_change 15-Sep-2000  
A:Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; A53788; A00844  
R:Yamada, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Oda, K.  
J. Biochem. 98, 1147-1156, 1985  
A:Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences  
A:Reference number: A91997; MUID:86111694  
A:Accession: A91997  
A:Molecule type: DNA  
A:Residues: 1-162, 'R', 164-512 <YU>  
A:Cross-references: GB:X03236; NID:939551; PIDN:CAA26981.1; PID:939552  
A:Experimental source: ATCC 27811  
R:Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindler, K.L.; Carmona, C.; Requena, J. Bacteriol. 166, 635-643, 1986  
A:Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus  
A:Reference number: A91817; MUID:86195857  
A:Accession: B24549  
A:Molecule type: DNA  
A:Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>  
A:Cross-references: GB:M3256; NID:9142510; PIDN:AAA22240.1; PID:9142511  
A:Experimental source: NCIB 8061  
R:Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.  
J. Bacteriol. 158, 369-372, 1984  
A:Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase  
A:Reference number: A91796; MUID:84185455  
A:Accession: A91796  
A:Molecule type: DNA  
A:Residues: 1-104 <STE>  
A:Cross-references: GB:K01984; NID:9142432; PIDN:AAA22193.1; PID:9142433  
R:Sibakov, M.; Palva, I.  
Eur. J. Biochem. 145, 567-572, 1984  
A:Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha  
A:Reference number: A21663; MUID:85076654  
A:Accession: A21663  
A:Molecule type: DNA  
A:Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D'  
A:Experimental source: Chromosomal DNA of ATCC 14580  
A:Note: The authors translated the codon CGT for residue 48 as Gly and GAC for residue  
R:Laide, B.M.; Chambliss, G.H.; McConnell, D.J.  
J. Bacteriol. 171, 2435-2442, 1989  
A:Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-inde  
A:Reference number: I39773; MUID:89213924  
A:Accession: I39774  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-29 <LAO>  
R:Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.  
Gene 96, 37-41, 1990  
A:Title: In vivo genetic engineering: homologous recombination as a tool for plasmid  
A:Reference number: I39772; MUID:91092499  
A:Accession: I39772  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA

```

||||| :||||| | ||||: ||: | |||||| | ||:|||| | ||||:|
Db 448 VANSGLAALITDPPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGFVNGSGVS 507
QY 481 VWVKQ 485
:|::
Db 508 IYVQR 512

RESULT 4
A24549
Alpha-amylose (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C:Date: 30-Jun-1998 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: A24549; I39501; I39770
J:Gray, G.L.; Mainzner, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona
R. J. Bacteriol. 166, 635-643, 1986
A:Title: Structural genes encoding the thermophilic alpha-amyloses of Baci
A:Reference number: A91817; MUID:86195857
A:Accession: A24549
A:Molecule type: DNA
A:Residues: 1-549 <GRA>
A:Cross-references: GB:M13255; NID:gl42512; PIDN:AAA22241.1; PID:gl42513
A:Experimental source: genomic DNA of strain NZ-3
R:Sato, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A:Title: Evidence for movement of the alpha-amylose gene into two phylogen
A:Reference number: I39501; MUID:88139156
A:Accession: I39501
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES>
A:Cross-references: GB:M29577; NID:gl42476; PIDN:AAA22235.1; PID:gl42478
A:Experimental source: strain Df-5
A:Accession: I39770
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 536-549 <RES2>

```

```

A:Experimental source: strain 799
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core h
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydro
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <MAG>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match          70.1%; Score 1900.5; DB 1; Length 549;
Best Local Similarity 68.6%; Pred. No. 1.2e-121;
Matches 328; Conservative 70; Mismatches 79; Indels 1; Gaps

Qy      6  NGTMMQYFEWHLPNDGHNHNRLLDAAENLKSKGITAVWIPPAKNGTSNDVGYGAYDLYD 65
Db      39  NGTMMQYFEWYLPDDGTLTWTKVANEANLSSLGITALLWLPAYKGTSRSDVGYGYDLYD 98

Qy      66  LGEFNQKGTVRTKTYGTRSQLOGAVTSLKNNGIQYGDVVMNHKGGADGTGMWAVEVNRS 125
Db      99  LGEFNQKGTVRTKTYGTRKQYLAQAAHAAGMOMYADVDFDHKGGADGTGMWAVEVNP 158

Qy      126  NRNOEISGEYTIKAWTKFDPGCRGNTSHNPKRWYHFDGTDWDSQLOLNKIKYKFGCTG 185
Db      159  DRNOEISGTQIQAWTKFDPGCRGNTYSSPKRWYHFDGVDWDSRKL-SRIYKFRGIG 217

Qy      186  AWDREVDITENGNDYLMYADTMDHPVIVNELRNWGVYVYTNLTLDGFRIDAVKHIKYSY 245

```

Db 218 ANDWEVDTEGNYDYLWYADLMDHDPVVTTELKNNWGWVYVNTTNDGFRDLDAVKHKFSF 277  
QY 246 TRDWLTHVRNTTCKPMPFAVEFKNDLAAIENYLNKTSNNHVSFVDPVPLHYNLYNASNSG 305  
Db 278 FPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTNTMSLFDAPLHNFYTASKSGG 337  
QY 306 YFDMNLINGSVOKRPHIAVTFVDNHDSDOPGSALESFVQSFKPLAYALILITREOGYPS 365  
Db 338 AFDMSTLMNTLMDKOPTLAVTFVDNHDTEPGALQSWDPWFKPLAYAFILITREOGYPC 397  
QY 366 VFYGDYGIPTGHPVSMKSKIDPLLOARTYAYGTQHDYFDHDIIGWTRGDSHPNSG 425  
Db 398 VFYGDYGIPTGHPVSMKSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGTEKPGSG 457  
QY 426 LATIMSDGPGGNKMYVKGKHAQVWRDITGNRSCTVTINADGWNFTVNGGAVSVWV 483  
Db 458 LAALITDGPGGKMWYVKGHAGKVFYDLTGNRSDTITNSDGGWGEFKVNGGVSVMV 515  
RESULT 5  
A24436  
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C;Species: Bacillus stearothermophilus  
C;Date: 05-Jun-1987 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C;Accession: A24436; I39777  
R;Nakajima, R.; Imanaka, T.; Alba, S.  
J. Bacteriol. 163, 401-406, 1985  
A;Reference number: A24436; MUID:85234394  
A;Accession: A24436  
A;Molecule type: DNA  
A;Residues: 1-549 <NAK>  
A;Cross-references: GB:M11450  
A;Experimental source: plasmid pAT5  
A;Note: amino end of the mature protein also determined  
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.  
Gene 96, 37-41, 1990  
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con  
A;Reference number: I39772; MUID:91092499  
A;Accession: I39777  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-45 <RES>  
A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515  
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the  
C;Genetics:  
A;Gene: amyS  
A;Genome: plasmid  
A;Start codon: GTG  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac  
F;1-34/Domain: signal sequence #status predicted <SIG>  
F;35-549/Product: alpha-amylase #status experimental <MAT>  
F;235-368/Domain: alpha-amylase core homology <AMY>  
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted  
F;268,298,365/Active site: Asp, Glu, Asp #status predicted  
Query Match 69.8%; Score 1894.5; DB 1; Length 549;  
Best Local Similarity 68.4%; Pred. No. 3e-121;  
Matches 327; Conservative 70; Mismatches 80; Indels 1; Gaps 1;  
QY 6 NGTMMQYFEWHLNPDGNHNRDLDAANKSGITAVWIPPAWKGTSQNDYGYGAYDLYD 65  
Db 39 NGTMMQYFEWYLPDGTTLTKVANEANLSSLGITALLPAPYKGTSRSDYGYGYDLYD 98  
QY 66 LGEFNOKGTVRTKYTRGSLQAGVTSLNKNGIQVYGVDMVHKGADCTGMVNAVEVNR 125  
Db 99 LGEFNOKGAVRTKYGTAKYQIAQIAHAAGMQVYADVDFDHKGADGTWWDVAVEVAPS 158

QY 126 NRNOEISGEYTIKAWTKFDFPGRGNTNHFKNRWYHFDGTDQSDRQLONKIYFRGTGK 185  
Db 159 DRNOEISGTQYQAWTKFDFPGRGNTYSGFKRWYHFDGVDWDESRKL-SRIYFRGTGK 217  
QY 186 ANDWEVDTEGNYDYLWYADLMDHDPVVTTELKNNWGWVYVNTTNDGFRDLDAVKHKFSF 245  
Db 218 ANDWEVDTEGNYDYLWYADLMDHDPVVTTELKNNWGWVYVNTTNDGFRDLDAVKHKFSF 277  
QY 246 TRDWLTHVRNTTCKPMPFAVEFKNDLAAIENYLNKTSNNHVSFVDPVPLHYNLYNASNSG 305  
Db 278 FPDWLSYVRSOTGKPLFTVGEYWSYDINKLHNYITKTNTMSLFDAPLHNFYTASKSGG 337  
QY 306 YFDMNLINGSVOKRPHIAVTFVDNHDSDOPGSALESFVQSFKPLAYALILITREOGYPS 365  
Db 338 AFDMSTLMNTLMDKOPTLAVTFVDNHDTEPGALQSWDPWFKPLAYAFILITREOGYPC 397  
QY 366 VFYGDYGIPTGHPVSMKSKIDPLLOARTYAYGTQHDYFDHDIIGWTRGDSHPNSG 425  
Db 398 VFYGDYGIPTGHPVSMKSKIDPLLIARDYAYGTQHDYLDHSDIIGWTRGTEKPGSG 457  
QY 426 LATIMSDGPGGNKMYVKGKHAQVWRDITGNRSCTVTINADGWNFTVNGGAVSVWV 483  
Db 458 LAALITDGPGGKMWYVKGHAGKVFYDLTGNRSDTITNSDGGWGEFKVNGGVSVMV 515  
RESULT 6  
ALBNS  
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens  
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C;Species: Bacillus amylioliquefaciens  
C;Date: 30-Nov-1980 #sequence\_revision 30-Jun-1987 #text\_change 18-Jun-1999  
C;Accession: A92389; A90307; I39756; I39763; A00843  
R;Takinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen  
J. Biol. Chem. 258, 1007-1013, 1983  
A;Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced  
A;Reference number: A92389; MUID:83108808  
A;Contents: PUB110  
A;Accession: A92389  
A;Molecule type: DNA  
A;Residues: 1-514 <YAK>  
A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA  
R;Chung, H.S.; Friedberg, F.  
Biochem. J. 185, 387-395, 1980  
A;Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.  
A;Reference number: A90307; MUID:80241725  
A;Accession: A90307  
A;Molecule type: protein  
A;Residues: 32-53, 'I', 55-63, 'L', 65-78, 'D', 80-93, 'S', 95-222 <CHU>  
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund,  
Gene 15, 43-51, 1981  
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region o  
A;Reference number: I39756; MUID:82051296  
A;Accession: I39756  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-96 <RES>  
A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298  
R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.  
Gene 59, 161-170, 1987  
A;Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its  
A;Reference number: I39763; MUID:88137952  
A;Accession: I39763  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-39 <RES>  
A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology  
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-514/Product: alpha-amylase #status predicted <MPT>



C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;200-333/Domain: alpha-amylase core homology <AMY>

Query Match\* 49.6%; Score 1347; DB 2; Length 493;  
Best Local Similarity 51.4%; Pred. No. 4e-84;  
Matches 247; Conservative 73; Mismatches 153; Indels 8; Gaps 3;

QY 6 NGTMMQYFEWHLFNDGNHNRRLDDAANKSKGITYAVWIPPAWKTSQNDVGYGAYDLYD 65  
DB 4 NHTMOMFEWHLAAGDGHKRLAEMAPELKAGIDFVWVPPVTKAVSAEDTGYGYDLYD 63  
QY 66 LGFENQKGTVRTKGYRSLQOGAVTSILKNGIQVYGDVVMNHKGGADGTEMVNAVEVNR 125  
DB 64 LGFEDQKGTVRTKGYRSLQOGAVTSILKNGIQVYGDVVMNHKGGADGTEMVNAVEVNR 123  
QY 126 NRNOEISGEYTIETAWTKFDPGGRNTHSNFKRWYHFDGTDWDSQROLQNKIYKFGTCK 185  
DB 124 DRTKEISEPTEIGWTFTFPGRQDQYSSFKWSEHFGTDFD-AREERTGVFRAGENK 182  
QY 186 ANDWEVDIENGNDYLMAYADIMDMHPEVINELRNWGVYVNTNLNLDGFRIDAVKHKISY 245  
DB 183 KWNENVDDEFGNDYLMFANIDYHNPVREMDWGWKLLDITLQCGGFRIDAIKHINHEF 242  
QY 246 TRDMLTHVRNTTGPMPFAVAFKNDLAATENYLNKTSWNHVSFVDPVPLHLYNLNNSGG 305  
DB 243 IKFEAAEMIRRGQDFYIVGEFWSNLDACREFLDTVQIDFVLSLHYKLHEASLGR 302  
QY 306 YFDMRNILNGSVQKHPHATVFDVNDHDSQPEALESFVQSWFKPLAYALILREQGYPS 365  
DB 303 FDFLSKIFDDILVQTHPHATVFDVNDHDSQPEALESWIGDFKPSAYALTLLRROGPV 362  
QY 366 VFYDGYGIGGPEYDVG---KKEILIDLLSARCNAKAYGEQEDYFDHANTIGWVRGVEEI 419  
DB 363 VFYDGYGIGGPEYDVG---KKEILIDLLSARCNAKAYGEQEDYFDHANTIGWVRGVEEI 419  
QY 422 PMSGLATMSDGPCKGKMYGKHKAGQVWRDITGNRSCTVTINADGNGFTVNGGAVSV 481  
DB 420 ESGGCAVVISNGDGEKRMFGEHRAGEVWDLTKSCDDQITIEDGWATPHVCGGVS 479  
QY 482 W 482  
DB 480 W 480

RESULT 9  
C86781  
A;Description: [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: C86781  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jalllon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
Genome Res. in press, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium.  
A;Reference number: A86625  
A;Accession: C86781  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-491 <STO>  
A;Cross-references: GB:AE005176; NID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: amyL  
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 41.8%; Score 1133; DB 2; Length 491;  
Best Local Similarity 43.0%; Pred. No. 1.4e-69;  
Matches 205; Conservative 96; Mismatches 172; Indels 4; Gaps 3;

QY 8 TMQMOMFEWHLFNDGNHNRRLDDAANKSKGITYAVWIPPAWKTSQNDVGYGAYDLYD 66  
DB 3 TILQAFWYLPDSQHNHNKENTPDLKGLFSGLWLPPLPASKASGVEDVGYGYDLYD 62

QY 67 GFENQKGTVRTKGYRSLQOGAVTSILKNGIQVYGDVVMNHKGGADGTEMVNAVEVNR 126  
DB 63 GFEDQKGTIPTTKYTKDEYLDLINTLHNNIEVYADIVFNHMMGADETETIADIKAE 122  
QY 127 RNOEISGEYTIETAWTKFDPGGRNTHSNFKRWYHFDGTDWDSQROLQNKIYKFGTCK 186  
DB 123 HLNIENNKTVETWTKFTFPGRQKDYDNVITWHTGTIDYE-RKNOEILEFE--GHE 179  
QY 187 WDMVEVDIENGNDYLMAYADIMDMHPEVINELRNWGVYVNTNLNLDGFRIDAVKHKISY 246  
DB 180 WDNVDSNNNFYLMAGADLDFSVSETVQLEKKGHWFSMTKIDGFRDLDAIKHIDEKYF 239  
QY 247 RDLTHVRNTTGPMPFAVAFKNDLAATENYLNKTSWNHVSFVDPVPLHLYNLNNSGGY 306  
DB 240 DKWLEQRAQLDRKLFIVGEYWSDDLKLEYLEQSSDRITQLDFVPLHFNKMEASSTGE 299  
QY 307 FDMRNILNGSVQKHPHATVFDVNDHDSQPEALESFVQSWFKPLAYALILREQGYPS 366  
DB 300 FDMRTLFDHTLTASQPELSVTFVDNHDITQEQALOSWIPANFKEHAYSLILLRKKETPV 359  
QY 367 FYDGYGIGGPEYDVG---KKEILIDLLSARCNAKAYGEQEDYFDHANTIGWVRGVEEI 426  
DB 360 FWGDLYGIPSHVNPVGDNLRTMIALRKDSSEFLRENDYFDHPDIIIGWTNLIKTDNKEYGL 419  
QY 427 ATIMSDGPGCKGKMYGKHKAGQVWRDITGNRSCTVTINADGNGFTVNGGAVSV 483  
DB 420 SCILTNKNGSKYMIIDKAYAGKYIIDLFGHREIPITLDQNGGAFFYVNDGVSVMV 476

RESULT 10  
B45738  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Species: Salmonella typhimurium  
C;Date: 07-Apr-1994 #sequence\_revision 18-Aug-1995 #text\_change 18-Jun-1999  
C;Accession: B45738  
R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.  
J. Bacteriol. 174, 6644-6652, 1992  
A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.  
A;Reference number: A45738; MUID:93015717  
A;Accession: B45738  
A;Molecule type: DNA  
A;Residues: 1-494 <RAH>  
A;Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045  
C;Genetics:  
A;Gene: amyA  
C;Function:  
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A;Pathway: glycogen/starch degradation  
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation  
F;202-335/Domain: alpha-amylase core homology <AMY>  
F;239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 38.8%; Score 1053; DB 1; Length 494;  
Best Local Similarity 42.1%; Pred. No. 3.8e-64;  
Matches 207; Conservative 84; Mismatches 183; Indels 18; Gaps 6;

QY 6 NGTMMQYFEWHLFNDGNHNRRLDDAANKSKGITYAVWIPPAWKTSQNDVGYGAYDLY 64  
DB 3 NPTLLQYFHYPPDGGKLSWELAEADGLNDIGINWVLPPLPCKGASGGYVGYDYDLYD 62  
QY 65 DLGLENQKGTVRTKGYRSLQOGAVTSILKNGIQVYGDVVMNHKGGADGTEMVNAVEVNR 124  
DB 63 DLGLEDQKGTATKYGDKRQLLTALDKNNIAVLDDVVVNHKMGADKERIRQVRNQ 122  
QY 125 SNRNOEISGEYTIETAWTKFDPGGRNTHSNFKRWYHFDGTDWDSQROLQNKIYKFG-- 182  
DB 123 DDRTOIDDDNIIECGWTRTYTFPARAGQYSNFIDWYHCFSGIDHIENPD-EDGIFKIVNDY 181  
QY 183 TCKANDWEVDIENGNDYLMAYADIMDMHPEVINELRNWGVYVNTNLNLDGFRIDAVKHK 242

Db 182 TCGWNDQVDDGNGFDYLMGENIDFRNHAHVTEIKYWARWYMEQTHCDGPRDLDAVKHIP 241  
QY 243 YSYTRDMLTHVRNTTCKPMFAVAEFKNDLAAIENLNKTSWNHVSFVDFVPLHYNLYNASN 302  
Db 242 AMFYKEWHEHQAQVAPKPLFVIAEYWSHEVDKQTYIDQVGEKTMFLDAPLQMKFHEASR 301  
QY 303 SGGYFDMRNLNGSVVQKHPIHAVTFVNDHDSOPGEALESFVQSWFKPLAYALILITREOG 362  
Db 302 QCAEYDMRHIFGTGLVEADPFHATVLANHDTPQLOALEAPVPEWFKPLAYALILIRENG 361  
QY 363 YPSVFYGDYGYGTPH-----GVPSMKSIDPLQARQTYAYGTQHDYDFDHHDTI 411  
Db 362 VPSVFYPDLYGASYEDSGENGETCRVDMFVI-NQLDRILARQREAHGIQTFLFDPHNCI 420  
QY 412 GHTRECDSSHPNSGLATIMSDGPGGNKMYGKHKAGQVWRDITGNRSCTVTINADGWN 471  
Db 421 AFSRSGTEENP--GCVVVLSNGDDGKTLILLGNDYANKTWRDFSGNROEYVVTNDGGEAT 478  
QY 472 FTVNGGAVSVWV 483  
Db 479 FTCNAGSVSVWV 490

## RESULT 11

A45738  
alpha-amylase (EC 3.2.1.1), cytosolic - Escherichia coli  
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase  
C:Species: Escherichia coli  
C:Date: 07-Apr-1994 #sequence\_revision 31-Oct-1997 #text\_change 18-Jun-1999  
R:Accession: D64956; A45738  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: D64956  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-495 <BLAT>  
A:CROSS-references: GB:AE000285; GB:U00096; NID:gl788229; PIDN:AAC74994.1; PID:gl788236;  
A:Experimental source: strain K-12, substrain MGL655  
R:Kana, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.  
J. Bacteriol. 174, 6644-6652, 1992  
A:Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.  
A:Reference number: A45738; MUID:9301517  
A:Accession: A45738  
A:Molecule type: DNA  
A:Residues: 1-18, 'SS', 21-108, 'V', 110-148, 'E', 150-233, 'I', 235-495 <RAH>  
A:CROSS-references: GB:L01642; NID:gl46021; PIDN:AAA23810.1; PID:gl46023  
C:Genetics:  
A:Gene: amyA  
C:Function:  
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A:Pathway: glycogen/starch degradation  
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
E:Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation  
F:202-335/Domain: alpha-amylase core homology <AMY>  
F:104,204,239/Binding site: calcium (Asn, Asn, His) #status predicted  
F:235,265,332/Active site: Asp, Glu, Asp #status predicted

Query Match 37.7%; Score 1022; DB 1; Length 495;  
Best Local Similarity 41.1%; Pred. No. 4.8e-62;  
Matches 202; Conservative 82; Mismatches 191; Indels 16; Gaps 5;  
QY 6 NCTMMQYFEWHLNPDGNHNRLRDDAANLKSIGITAVIPPAWKGTSON-DVGYGAYDLY 64  
Db 3 NPTLLQCFHWYYPPEGKLPWELAEADGNDGINNWLPPAYKASGGYSGYDSYDLF 62  
QY 65 DLGEFNQKGTVRTKTYKTRSQLQAVTSLKNGIQVYGVVMMHKGADGTEMVNAVEVNR 124  
Db 63 DLGEFDQKGSIPTKYGDKVQLLAAIDALKRNDIAVLDDVVVNHKMGADKEAIRQVRNA 122

QY 125 SNRNOEISEYETIAWTKFDFPGRGNTHSNPKRWYHFDGTDWDOSRQLOKNIYKFRG-- 182  
Db 123 DORTQIDEEIECEGTRITFTPARAGQYSQFIWDFKCFSGIDHIENPD-EDGIFKIVNDY 181  
QY 183 TCKAWDEWDIENGNDYILMYADIDMDHPEVINELRNMGVWYTNLTNLDFRIDAVKHKH 242  
Db 182 TCEGWNQVDDGNGFDYLMGENIDFRNHAHVTEIKYWARWYMEQTHCDGPRDLDAVKHIP 241  
QY 243 YSYTRDMLTHVRNTTCKPMFAVAEFKNDLAAIENLNKTSWNHVSFVDFVPLHYNLYNASN 302  
Db 242 AMFYKEWHEHQAQVAPKPLFVIAEYWSHEVDKQTYIDQVGEKTMFLDAPLQMKFHEASR 301  
QY 303 SGGYFDMRNLNGSVVQKHPIHAVTFVNDHDSOPGEALESFVQSWFKPLAYALILITREOG 362  
Db 302 MGRDMDTQIFGTGLVEADPFHATVLANHDTPQLOALEAPVPEWFKPLAYALILIRENG 361  
QY 363 YPSVFYGDYGYGTPHGVPS-----MKSIDPLQARQTYAYGTQHDYDFDHHDTI 412  
Db 362 VPSVFYPDLYGASYEDVGGDGTYPIDMPILBQLDELILARQFAHQVQTLFFDHPNCIA 421  
QY 413 WTRREGDSSHPNSGLATIMSDGPGGNKMYGKHKAGQVWRDITGNRSCTVTINADGWN 472  
Db 422 FSRSGTEENP--GCVVVLSNGDDGKTLILLGNDYANKTWRDFSGNROEYVVTNDGGEAT 478  
QY 473 TVNNGGAVSVWV 483  
Db 480 FCNAGSVSVWV 490

## RESULT 12

B85810  
cytoplasmic alpha-amylase [imported] - Escherichia coli (strain O157:H7)  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
C:Accession: B85810  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: B85810  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-495 <STO>  
A:CROSS-references: GB:AE005174; NID:gl2516028; PIDN:AAG56942.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: amyA  
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 37.1%; Score 1006; DB 2; Length 495;  
Best Local Similarity 40.7%; Pred. No. 5.9e-61;  
Matches 200; Conservative 83; Mismatches 192; Indels 16; Gaps 5;  
QY 6 NCTMMQYFEWHLNPDGNHNRLRDDAANLKSIGITAVIPPAWKGTSON-DVGYGAYDLY 64  
Db 3 NPTLLQCFHWYYPPEGKLPWELAEADGNDGINNWLPPAYKASGGYSGYDSYDLF 62  
QY 65 DLGEFNQKGTVRTKTYKTRSQLQAVTSLKNGIQVYGVVMMHKGADGTEMVNAVEVNR 124  
Db 63 DLGEFDQKGSIPTKYGDKVQLLAAIDALKRNDIAVLDDVVVNHKMGADKEAIRQVRNA 122  
QY 125 SNRNOEISEYETIAWTKFDFPGRGNTHSNPKRWYHFDGTDWDOSRQLOKNIYKFRG-- 182  
Db 123 DORTQIDEEIECEGTRITFTPARAGQYSQFIWDFKCFSGIDHIENPN-EDGIFKIVNDY 181  
QY 183 TCKAWDEWDIENGNDYILMYADIDMDHPEVINELRNMGVWYTNLTNLDFRIDAVKHKH 242  
Db 182 TCEGWNQVDDGNGFDYLMGENIDFRNHAHVTEIKYWARWYMEQTHCDGPRDLDAVKHIP 241  
QY 243 YSYTRDMLTHVRNTTCKPMFAVAEFKNDLAAIENLNKTSWNHVSFVDFVPLHYNLYNASN 302



Db 242 AWFYKEMIEHVEAPKPLFVIAEYWSHEVDKLOTIDQVEGKTMDFDAPLQMKFHEAR 301  
QY 303 SGGYFDMNRNLINGSVQKHPHIAVTFVDNHDSPGEALSFVQSWFKPLAYALILPREQG 362  
Db 302 MGRNYDMTQFTGLVEADFXHVTXVANHDTQXLALEAPVFPWFKPLAYALILLRENG 361  
QY 363 YPSVFFGDDYGIPTHGVPSS-----MKSIDPLQARQYAYCTQHDYFDHDDIIG 412  
Db 362 VPSVFYDLGCAHYEDVGGDGQYTPIDMPIIEQLDELILARQFAHGVSQVLFDFHPNCLIA 421  
QY 413 WTRGDSHNSGLATIMDPGNGKMYGKHKAGQVWRDITGNRSQGTIVTINADGNGNF 472  
Db 422 FSRSGTDEYP--GCVVMSNGDDGEXTIHLGENYGNKTRDFLGNROESVVTDENGEATF 479  
QY 473 TVNGGAVSVWV 483  
Db 480 FCNGGVSVMV 490  
  
RESULT 13  
A:Species: Bacillus amyloliquefaciens (fragments)  
C:Date: 05-Jun-1987 #sequence,revision 05-Jun-1987 #text\_change 31-Mar-2000  
C:Accession: A91760; A91759; A19506  
R:Sachdev, O.; Friedberg, F.  
A:Reference number: A91760; MUID:82189140  
A:Accession: A91760  
A:Molecule type: protein  
A:Residues: 1-56;57-144 <SAC>  
A:Note: residues 1-56 correspond to residues 229-287 of the complete sequence; residues  
R:Detert, S.D.; Friedberg, F.  
A:Reference number: A91760; MUID:82189140  
A:Accession: A91760  
A:Molecule type: protein  
A:Residues: 145-217 <DET>  
A:Note: this sequence corresponds to residues 398-469 of the complete sequence  
C:Comment: See PIR:ALBSN.  
C:Function:  
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
A:Pathway: glycogen/starch degradation  
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 14.5%; Score 393.5; DB 2; Length 217;  
Best Local Similarity 34.3%; Pred. No. 8e-20;  
Matches 94; Conservative 32; Mismatches 49; Indels 99; Gaps 9;  
  
QY 203 YADIDMDHPEVINELRNNGVWYTNFLNLDGFRIDAKHKIKYSYTRDMLTHVRNTTGKPMF 262  
Db 1 YADVDDYDPDVVAETKKGRLMTASQLHLDG---KAVVTQPK----- 39  
  
QY 263 AVAEFWKNDLAAIENYLAKTSWNHVSFVDFPLHYNLYNASNGGYFDMNRNLINGSVQKHP 322  
Db 40 -----AVHIAEFSEAKVQGHT--MHRLLDGTVYSRHP 69  
  
QY 323 IHAVTFVDNHDSPGEALSFVQSWFKPLA-----Y 353  
Db 70 EKAVEFVENTESLPGH-----FKPLSVDTGRLPNDEALSDGFTLQTHQFKAYW 120  
  
QY 354 ALILPREQ--GYPSVFYGDY---YGIPTHG-----VPSMKSIDPLQARQYAYCTQHDY 404  
Db 121 AFILREESGYQVQYGVGVESGYMGTCTSPKEIPSLKDNIEPILKARKEYAYGQHDY 180  
  
QY 405 FPDHDIIGWTRGDSHNSGLATIMSDPGNGK 438  
Db 181 IDPH-VIGWTRGDSAAKSGLAALISDGPGGK 213

RESULT 14  
A29130  
beta-amylase (EC 3.2.1.2) / alpha-amylase (EC 3.2.1.1) precursor - Bacillus polymyxa  
C:Species: Bacillus polymyxa  
C:Date: 25-Oct-1987 #sequence,revision 03-Mar-1994 #text\_change 15-Oct-1999  
C:Accession: A29130; B29130; A32251; A29108  
R:Kawazu, T.; Nakanishi, Y.; Uozumi, N.; Sasaki, T.; Yamagata, H.; Tsukagoshi, N.; Ud  
J. Bacteriol. 169, 1564-1570, 1987  
A:Title: Cloning and nucleotide sequence of the gene coding for enzymatically active  
A:Reference number: A29130; MUID:87165765  
A:Accession: A29130  
A:Molecule type: DNA  
A:Residues: 1-936 <KAW>  
A:Cross-references: GB:M15817  
A:Experimental source: strain 72  
A:Accession: B29130  
A:Molecule type: protein  
A:Residues: 36-50 <KA2>  
R:Uozumi, N.; Sakurai, K.; Sasaki, T.; Takekawa, S.; Yamagata, H.; Tsukagoshi, N.; Ud  
J. Bacteriol. 171, 375-382, 1989  
A:Title: A single gene directs synthesis of a precursor protein with beta- and alpha-  
A:Reference number: A32251; MUID:89123046  
A:Accession: A32251  
A>Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 937-1196 <UOZ>  
A:Experimental source: strain 72  
R:Rhodes, C.; Strasser, J.; Friedberg, F.  
Nucleic Acids Res. 15, 3934, 1987  
A:Title: Sequence of an active fragment of B. polymyxa beta amylase.  
A:Reference number: A29108; MUID:87231094  
A:Accession: A29108  
A:Molecule type: DNA  
A:Residues: 'MIGI', 2-66, 'S', 68-99, 'D', 101-153, 'N', 155-176, 'Q', 178-226, 'KS', 229-329, 'S  
'K', 737-740, 'S', 742-757, 'N', 759-776 <RHO>  
A:Experimental source: ATCC 8523  
C:Genetics:  
A:Start codon: TTG  
C:Function:  
A:Description: catalyzes both the hydrolysis of internal 1,4-alpha-D-glucosidic bonds  
vely from the non-reducing end (beta-amylase activity)  
A:Pathway: glycogen/starch degradation  
C:Superfamily: alpha-amylase core homology  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation  
F:1-35/Domain: signal sequence #status predicted <SIG>  
F:36-1196/Product: beta-amylase/alpha-amylase #status predicted <MAT>  
F:908-1033/Domain: alpha-amylase core homology <AMT>  
  
Query Match 11.6%; Score 315; DB 2; Length 1196;  
Best Local Similarity 24.1%; Pred. No. 1.6e-13;  
Matches 125; Conservative 67; Mismatches 189; Indels 138; Gaps 25;  
  
QY 1 HHNGTGTMTQYFVHPLPNDGNHNRLRDDAANLKSGITAVWIPPAWKGTSDNV--GYG 59  
Db 766 NYGFNSNNSDQKWH-----GGDFQGIINKLDYIKNGFTAITWITPTVMQSEYAYHGYH 821  
  
QY 60 AYDIYLDGEFNQKGTVTKYTRTSQLOGAVTSLKNGIQYGVVNMHKGADGTEMVNA 119  
Db 822 TYDFY-----AVDGHGTMKDLQELVRAKHDKNIAVMVDVVVNHG----- 862  
  
QY 120 VEVNRSNRNQBISGEYTTAEWTKFDF--PGRGNTHSNF--KRWYHFDG--TDWDQSRLQN 175  
Db 863 -----DFQPGNGFAKAPDKADWYHHNGDITDGDYNSNQ-- 897  
  
QY 176 KIYFERGTGKAWDEVDIENGNYDLYMTADTMDHPEVINELRNNGVWYTNFLNLDGFR 235  
Db 898 -----WK--IENG--DVAGLDLLENHENPATANELKNWIKLLNETGIDGLRL 940  
  
QY 236 DAVKHIKYSYTRDMLTHVRNTTGKPMFAVAFWKNDLAAIENYLAKTSWNHVSFVDFPLHY 295  
Db 941 DTVKHPKGFLLKDF--DQAANT-----FTMGELFHCDPAVVDY---TRYLDAALDFPMY 991



```

Db      l:l: | | | : | | | : | | | : | | | : | | | :
408 WDDTFYAFQSYNGDEVVVMNNWSNSQTFTVPNIDRVANGQTLYNMGTDKVTYNGS 467

Qy      479 VS 480

Db      ::::
468 IT 469

Search completed: November 28, 2001, 16:59:03
Job time: 196 sec
```

Search completed: November 28, 2001, 16:59:03  
Job time: 196 sec

```

Query Match      11.2%; Score 304.5; DB 2; Length 482;
Best Local Similarity 24.1%; Pred. No. 2.5e-13;
Matches 116; Conservative 62; Mismatches 171; Indels 133; Gaps 24;

Qy 34 LKSGITAVWIPPAWKTSONDV--GYGAYDLYDLGEFNQKGTVRTKYKTRSOLOQAVTSL 92
   : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 86 IKNGFTAIWITPVTMQKSANAYHYTYDFY-----SVDGHLGSMAKLQELVRAA 136

Qy 93 KNGGIQYGVVVMHKGAGDGTENVNAVVENRNRNOEISGEYITIAWKTFDFPGRGNTH 152
   | | | | | | | | | | | | | | | | | | : | : | : | : | : | : | :
Db 137 HAKGISVMLDVVAANH-----TGDFQSPSFAPKD-----166

Qy 153 SNFKRWYHF--DGTDMQSRQLQNKYKFRGTCKAMDWEVDIENGNYDLYMAYADIDMDH 210
   : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 167 ---KADMYHHYGDQDWNQ-----W-W--VENG--DIAGLDDLQNQN 201

Qy 211 PEVINELRNGGVVNTNLNLDGFDVIDAVKHKKYSYTRDMLTHVRNTTKCPMFAVAEPKN 270
   : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 202 PAVATELKNITAMIVQTTGVDGLRVDVTPKPKWFNREF--DGAANT-----FTLGEVFHG 255

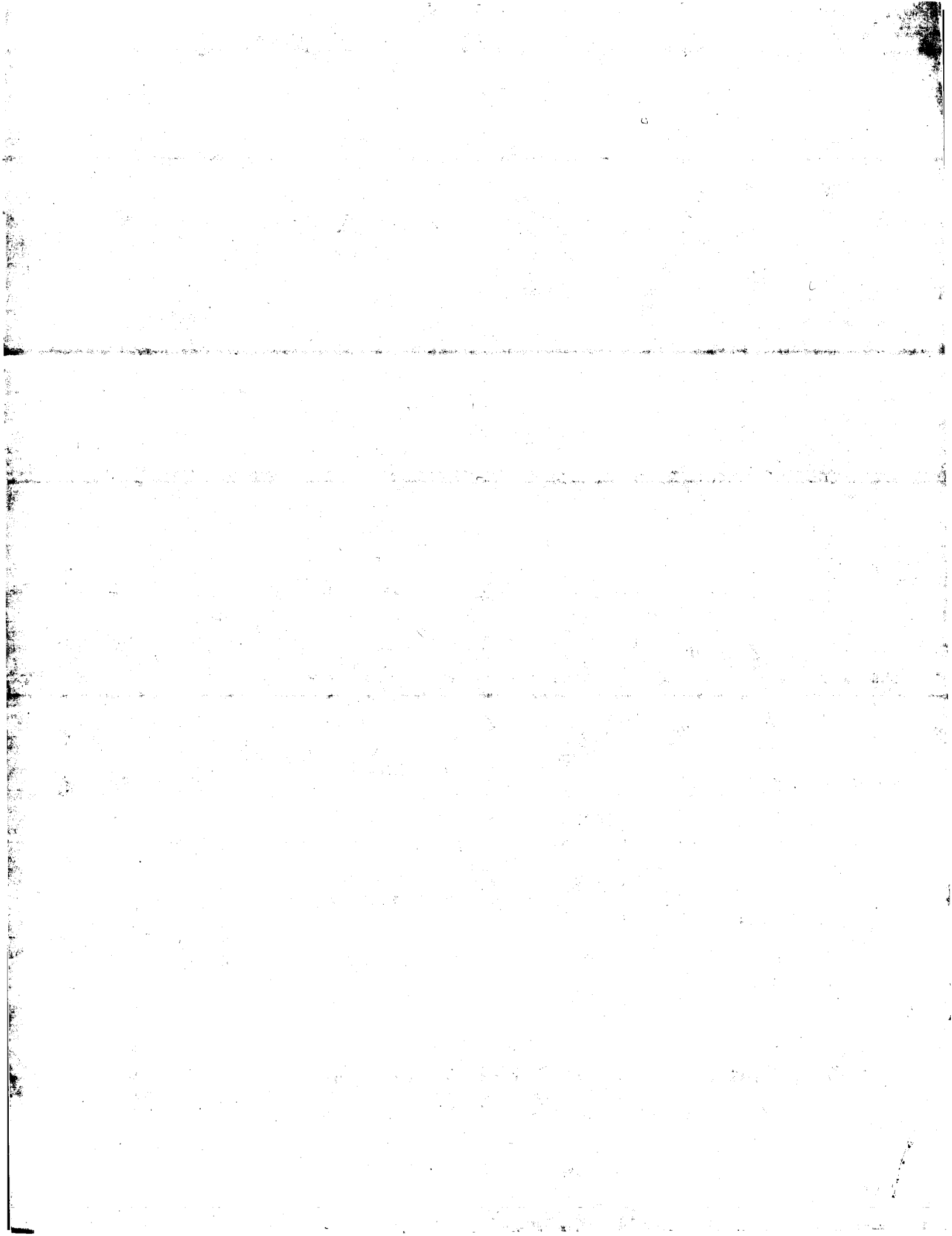
Qy 271 DLAAIENYLNKTSWNHSYFVDVPLHYLNYSNCSGGYFDMRNLILGVSVQ---KHPIHAVT 327
   : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 256 DPAVGDY---TNLYDAVLDPMYITTKNV--FGQDSMRTIADRYAODYRYKKNPWINGL 310

Qy 328 FVDNHD-----SQPGEALESFVGSWFKPLAYALILIREQYSPSVFYGDYGIPIHG 378
   | : | | | : | | : | | : | | : | | : | | : | | : | | : | | :
Db 311 FIDNHDPVREFLNEASGKPGASWDKWQP--LKAALGFMFTTR--GIPILYQCTEQG-----361

Qy 379 VPSMKSITDPLQARQYVAYCTQHDYFDHDDIIGWTRGDSHSPNSGLATIMSDPGPGNK 438
   | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 362 ---FSGGADP--YNRDDWVFNKDHKLGYIAKLNYIR-----NTHVA---LRGTQAEK 407

Qy 439 WM-----YVGKHKAGQV---WRDITGN-----RSGTVTIINADGNGFETVNGGA 478

```



OM of: US-09-590-375-2 to: Issued\_Patents\_NA:\* out\_format : pfs  
Date: Nov 28, 2001 5:38 PM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framet\_p2n.model -DEV=xlh  
-O/cgn2\_1/USPTO.spool/US09590375/runat\_28112001\_152038\_21070/app\_query.fasta\_1.1092  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000  
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FCGAPOP=6.000 -FCGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM-ext -MINLEN=0 -MAXLEN=2000000000  
-USER=US09590375.cgn1\_1\_107 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-590-375-2  
Query length: 485  
Database: Issued\_Patents\_NA:\*  
Database sequences: 351203  
Database length: 113238999  
Search time (sec): 64.100000

score\_list:

Sequence	Strd Orig	zScore	Escore	Len	Documentation
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-446-803-4		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-861-837-4		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-600-656-4		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-9		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-14		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-193-068-9		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-193-068-13		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-9		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-13		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-354-191A-4		2613.00	2613.00	4886.90	1.5e-264 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-600-908A-11		2613.00	2613.00	4886.87	1.5e-264 1458
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-683-838A-11		2613.00	2613.00	4886.87	1.5e-264 1458
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-446-803-5		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-861-837-5		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-600-656-5		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-10		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-15		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-193-068-10		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-193-068-14		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-10		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-14		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-354-191A-5		2440.00	2440.00	4561.40	2.0e-246 1455
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-600-656-6		1910.50	1910.50	3562.47	6.8e-191 1548
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-11		1910.50	1910.50	3564.47	6.8e-191 1548
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-193-068-11		1910.50	1910.50	3564.47	6.8e-191 1548
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-11		1910.50	1910.50	3564.47	6.8e-191 1548
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-354-191A-6		1910.50	1910.50	3562.67	6.8e-191 1548
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-720-899-5		1910.50	1910.50	3562.67	8.6e-191 1814
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-459-610-5		1910.50	1910.50	3562.67	8.6e-191 1814
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-343-804-5		1910.50	1910.50	3562.67	8.6e-191 1814
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-687-399-5		1910.50	1910.50	3562.67	8.6e-191 1814
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-600-908A-5		1910.50	1910.50	3562.67	8.6e-191 1814
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-683-838A-5		1910.50	1910.50	3562.67	8.6e-191 1814
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-182-859-5		1910.50	1910.50	3562.67	8.6e-191 1814
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-146-422-33		1909.00	1909.00	3560.08	1.2e-190 1777
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-253-575-1		1909.00	1909.00	3560.08	1.2e-190 1777
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-626-554-16		1909.00	1909.00	3560.08	1.2e-190 1777
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-814-052-7		1909.00	1909.00	3559.36	1.3e-190 1893
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-812-829-7		1909.00	1909.00	3559.36	1.3e-190 1893
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-264-097-1		1909.00	1909.00	3559.21	1.3e-190 1918

/cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-720-899-1 + 1909.00 3559.20 1.3e-190 1920  
/cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-459-610-1 + 1909.00 3559.20 1.3e-190 1920  
/cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-343-804-1 + 1909.00 3559.20 1.3e-190 1920  
/cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-687-399-1 + 1909.00 3559.20 1.3e-190 1920  
/cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-600-908A-1 + 1909.00 3559.20 1.3e-190 1920

seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-446-803-4

seq\_documentation block:

; Sequence 4, Application US/08446803  
; Patent No. 5824531  
; GENERAL INFORMATION:  
; APPLICANT: Ottrup, Helle  
; APPLICANT: Bisgaard-Frantzen, Henrik  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Rasmussen, Michael Dolberg  
; APPLICANT: Van Der Zee, Pia  
; TITLE OF INVENTION: Alkaline Bacillus Amylase  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: No. 5824531 No. 5824531disk of No. 5824531th America  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,803  
; FILING DATE: 01-June-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: 38,711  
; REFERENCE/DOCKET NUMBER: 4157.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 867-0123  
; TELEFAX: (212) 878-9655  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1455 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-446-803-4

alignment\_scores:  
Quality: 2613.00 Length: 485  
Ratio: 5.421 Gaps: 0  
Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x US-08-446-803-4 ..

Align seg 1/1 to: US-08-446-803-4 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyRPhesGluTrpHisLe 17  
|||||  
1 CATCAATGGAACAAATGGTACTATGATGCAATATTTCAATGGTATT 50  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34  
|||||  
51 GCCAATGACGGGAATCATTTGGACAGGTTGAGGATGACGACGTAAC 100  
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50  
|||||  
101 TAAAGAGTAAGGGATAACAGCTGTATGATGCCACCTGCATGGAAGGG 150

351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
1051 CTTGCATATGCTGGTTCGACAAAGGGAACAAGGTTATCTTCCTGAT 1100  
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384  
1101 TTATGGGGATTACTACGGTATCCCAACCCATGGTGTTCGGCTATGAAT 1150  
384 eTyrGlyAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
1151 CTAAATAGACCCCTCTTCGAGGACGCTCAAACTTTTGCCTATGGTACG 1200  
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrPheArgGluG 417  
1201 CAGCATGATTACTTTGATCATCATGATATATTCGTTGGACAAGAGAGG 1250  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
1251 AAATAGCTCCCATCCAAATTCAGGCTTTCAGCCATTCATGTCAGATGTC 1300  
434 tGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
1301 CAGGTGGTAACAAATGGATGTATGTGGGAAAAATAAAGCGGACAGTT 1350  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
1351 TGGAGAGATATTACCGGAAATAGGACAGCCGTCACAAATTAATGCAGA 1400  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484  
1401 CGATGGGGTAATTTCTCTGTTAATGGAGGTCCTTCGTTTGGGTGA 1450  
484 ysGln 485  
1451 AGCAA 1455

seq\_name: /cogn\_6/ptodata/2/ina/5B\_COMB.seq:US-08-861-837-4

seq\_documentation\_block:  
; Sequence 4, Application US/08861837  
; Patent No. 5856164

GENERAL INFORMATION:

APPLICANT: Ottup, Helle  
APPLICANT: Bisgaard-Frantzen, Henrik  
APPLICANT: Ostergaard, Peter Rabbek  
APPLICANT: Rasmussen, Michael Dolberg  
APPLICANT: Van Der Zee, Pia  
TITLE OF INVENTION: Alkaline Bacillus Amylase  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: No. 58561640 No. 5856164disk of No. 5856164th America  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10174

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,837  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,803  
FILING DATE: 01-June-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: 38,711  
REFERENCE/DOCKET NUMBER: 4157.204-US  
TELECOMMUNICATION INFORMATION:

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67  
151 ACTTCCCAAGATGCTAGGTTATGGAGCCTATGATTTATATGATCTTGG 200  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
201 AGAGTTTAAACCAAGAGGACGGTTCGTACAAATATGGAACACCAACC 250  
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
251 AGCTACAGGCTGGGTGACCTCTTTAAAAAATAACGGCATTCAGGTATAT 300  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
301 GGTGATGCTGCTATGAATCATAAAGTGGAGCAGATGGTACGGAATGT 350  
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
351 AAATGGGTAGAACTGAAATCGGAGCAACCGAAACACCAAGAACTCAGGAG 400  
134 luTyrThrIleGluAlaIatrpThrLysPheAspPheProGlyArgGlyAsn 150  
401 AGTATGCAATAGAGCCTGGACAAAGTTGATTTCTCGAAGAGGAAAT 450  
151 ThrHisSerAsnPheLysTyrArgTyrPheAspGlyThrAspTr 167  
451 AACCATTCACAGCTTTAAGTGGCCTGGTATCATATTTGATGGGACATG 500  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
501 GGATCAGTCAGCCAGCTTCAAAACAAATATATATAATTCAGGGGAACAG 550  
184 lyLysAlaIatrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
551 GCAAGGCTGGGACTGGGAATGATACAGAGAAATGCAACTATGACTAT 600  
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
601 CTTATGTATGCAGACGTTGGATATGGATCCCAAGCAAGTAATACATGA 650  
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
651 TAGAACTGGGGAGTGGTATACGAATACACTGAACCTTTGATGGATT 700  
234 rGlyeAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
701 GAATAGATGCAAGTGAACATATAAATATAGCTTTACGAGAGATGGCTT 750  
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
751 ACACATGTGCGTAACACCAAGGTAAACCAATGTTTCAGTGGCTGAGTT 800  
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
801 TTGAAAAATGACCTTGGTGAATGAAACTATTGTAATAAAAACAAGTT 850  
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
851 GGAATCATCGGTGTTGATGTTCTCTCCACTATAATTTGTACAATGCA 900  
301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
901 TCTAATAGCGGTGTTATATGATATGAAATATTTTAAATGTTCTGT 950  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
951 GGTGCAAAACATCCACACATGCGCTTACCTTTGTTGTAACCATGATT 1000  
334 eGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
1001 CTCAGCCCGGGAAGCATTTGGAATCCTTTGTTCAACAATGTTTAAACCA 1050

```

;
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-861-837-4

```

## alignment\_scores:

```

Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

```

## alignment\_block:

```

US-09-590-375-2 x US-08-861-837-4 ..
Align seg 1/1 to: US-08-861-837-4 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
1 CATCATTAATGGGAACAAATGGTACTATGATGCAATATTTGCAATGGTATT 50
17 uProAsnAspGlyAsnHisTriPAsnArgLeuArgAspAspAlaAlaAsnL 34
11111111111111111111111111111111111111111111111111111
51 GCCAATGACGGGATCATTTGGNACAGGTTGAGGGATGACGACGCTAACT 100
34 euLysSerLysGlylleThrAlaValTrpIleProAlatrPlyGly 50
11111111111111111111111111111111111111111111111111111
101 TAAAGAGTAAAGGATAACAGCTGTATGGATCCACCTCATGGAAGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTrpAspLeuGl 67
11111111111111111111111111111111111111111111111111111
151 ACTTCCCAAGATGATAGCTTATGAGCCTATGATTTATATGATCTTGG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
11111111111111111111111111111111111111111111111111111
201 AGAGTTTACCAGAGGAGGCGGTTCGTACAAAATATGGAACACGCAACC 250
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlylleGlnValTyr 100
11111111111111111111111111111111111111111111111111111
251 AGCTACAGGCTGGGTGACCTCTTTAAAAAATAACGGCATTCAGGTATAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrClnuMetVa 117
11111111111111111111111111111111111111111111111111111
301 GGTGATGTCGTCAATGAATCATAAAGGTGGAGCAGATGGTACGGAAATGT 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
11111111111111111111111111111111111111111111111111111
351 AAATGCGGTAGAGTCAATCGGAGCAACCGAAACAGGAACCTCAGGAG 400
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
11111111111111111111111111111111111111111111111111111
401 AGTATGCAATAGAGCGGTGACAAAGTTTGATTTCTCTGGAAGAGGAAT 450
151 ThrHisSerAsnPhelysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
11111111111111111111111111111111111111111111111111111
451 AACCATTCAGCTTTAAAGTGGCGCTGGTATCATATTTTGGTGGGACAGTT 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
11111111111111111111111111111111111111111111111111111
501 GGATCAGTCACGCCACCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
11111111111111111111111111111111111111111111111111111
551 GCAAGGCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
11111111111111111111111111111111111111111111111111111
601 CTTATGATGCAGACGCTGGATGATGATGATCACCACCAAGAGTAATACATGA 650

```

```

217 uArgAsnTriPValTriPValTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
11111111111111111111111111111111111111111111111111111
651 TAGAAACTGGGAGTGTGTATACGAATACACTGAACCTTGATGGATTTA 700
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
11111111111111111111111111111111111111111111111111111
701 GAATAGATGCAGTGAACATATATAAATATAGCTTTACGAGAGATTGGCTT 750
251 ThrHisValArgAsnThrThrGlyLysPrometPheAlaValAlaGluPh 267
11111111111111111111111111111111111111111111111111111
751 ACACATGTGCGTAACACACAGCTAAACCAATGTTTGCAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
11111111111111111111111111111111111111111111111111111
801 TTGGAATAATGACCTTGGTGCATTTGAAACTATTTGAATAAACAAGTT 850
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
11111111111111111111111111111111111111111111111111111
851 GGAATCACCTCGGTGTTGATGTTCTCTCCACTATAAATTTGTACAATGCA 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
11111111111111111111111111111111111111111111111111111
901 TCTAATAGCGGTGTTTATATGATATGAGAAATATTTTAAATGGTCTGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
11111111111111111111111111111111111111111111111111111
951 GGTGCAAAAACATCCAAACACATGCCGTACTTTTGTGTATAACCATGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
11111111111111111111111111111111111111111111111111111
1001 CTCAGCCCGGGGAAGCATTTGGAATCCTTTTCAACAATAGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
11111111111111111111111111111111111111111111111111111
1051 CTTGCAATATGATGCTGTTCTGCAAGGAAACAAGGTTATCCTTCCGTATT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
11111111111111111111111111111111111111111111111111111
1101 TTATGGGATTACTACGGTATCCCAACCCATGGTGTCCGGCTATGAAT 1150
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
11111111111111111111111111111111111111111111111111111
1151 CTAAAAATAGACCTCTCTCGAGGCAGCTCAAACTTTTGCCTATGCTAGC 1200
401 GlnHisAspTyrPheAspHisHisAspIleGlyTrpThrArgGluGl 417
11111111111111111111111111111111111111111111111111111
1201 CAGCATGATTACTTTGATCATCATGATATATCGTTGGACAAGAGAGGG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
11111111111111111111111111111111111111111111111111111
1251 AAATAGCTCCCATCCAAATTCAGSCCTTGCACCATTTATGTCAGATGTC 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
11111111111111111111111111111111111111111111111111111
1301 CAGGTGGTAAACAATGATGATATGTGGGAAAAAATAAAGCGGACAAAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
11111111111111111111111111111111111111111111111111111
1351 TGGAGAGATATTACCGGAAATAGGACAGCGCCGTCACAATTAATGCGAGA 1400
467 pGlyTyrGlyAsnPhethrValAsnGlyGlyAlaValSerValTrpVal 484
11111111111111111111111111111111111111111111111111111
1401 CGGATGGGTAAATTTCTCTGTTAATGGAGGTCGCTTCGGTTTGGGTGA 1450
484 ysgln 485
11111111111111111111111111111111111111111111111111111
1451 AGCAA 1455

```

seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:US-08-600-656-4

seq\_documentation\_block:

; Sequence 4, Application US/08600656

Thu Nov 29 10:43:47 2001

```

; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,656
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Landiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-600-656-4

alignment_scores:
  Quality: 2613.00      Length: 485
  Ratio: 5.421          Gaps: 0
  Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:
  US-09-590-375-2 x US-08-600-656-4  ..

Align seg 1/1 to: US-08-600-656-4 from: 1 to: 1455

  1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
  |||||
  1 CAICNTAATGGACAAATGGTACTATGATGCAATATTTGCAATGGTATT 50
  |||||
  17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAsnL 34
  |||||
  51 GCCAAATGACGGGAATCATTTGGACAGGTGAGGGATGACGCACGTA 100
  |||||
  34 euLysSerLysGlyLeuAlaValTrpIleProProAlaTrpLysGly 50
  |||||
  101 TAAAGATTAAGGGATCAACAGCTGATGGATCCACCTGCATGGAAGGG 150
  |||||
  51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTrpAspLeu 67
  |||||
  151 ACTTCCCAAGATGATGATGGTATGGAGCCCTATGATTTATGATCTGG 200
  |||||
  67 yCluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSer 84
  |||||
  201 AGAGTTTAAACAGAGGGGCGGTTCGTACAAAATATGGAACACGCAAC 250
  |||||
  84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
  |||||
  251 AGCTACAGGCTCGGTGACCTCTTTAAATAAATACGGCATTTCAGGTAT 300
  |||||
  101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
  |||||
  301 GGTGATGTCGTCATGAATCAATAAGGTGGAGCAGATGGTACGGAATTT 350
  |||||
  117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134
  |||||
  351 AAATCGCGTAGAAGTGAATCGGAGCAACCCGAAACAGGAAACCTCAGG 400
  |||||
  134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
  |||||
  401 AGTATGCAATAAGACCGTGGACAAGTTTGATTTCTCGGAAGAGGAAT 450
  |||||
  151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
  |||||
  451 AACCATTCACGCTTTAAGTGGCGTGTATCATTTTGTATGGACAGATTG 500
  |||||
  167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
  |||||
  501 GGATCAGTCACGCCAGCTTCAAAACAAATATATAAATTCAGGGGAACAG 550
  |||||
  184 lYlSalatTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
  |||||
  551 GCAAGCGCTGGGACTGGGAAGTCGATACAGAGATGCAACTATGACTAT 600
  |||||
  201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
  |||||
  601 CTTATGATGCAGACGTGGATATGATGATGCAACTGAACTTATACATGAA 650
  |||||
  217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
  |||||
  651 TAGAACTGGGGAGTGGTGTATACGAATACACTGAACTTGTATGGATT 700
  |||||
  234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
  |||||
  701 GAATAGATCAGTGAACATATATAAATATAGCTTACGAGAGATTGGCTT 750
  |||||
  251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
  |||||
  751 ACATGTCGCTAACACACACAGGTAAACCAATGTTTGCAGTGGCTGAGT 800
  |||||
  267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
  |||||
  801 TTGGAAAAATCAGCTTGGTGCAATGAAACTATTTGAATAAAACAAGTT 850
  |||||
  284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
  |||||
  851 GGAATCACTCGGTGTTGATGTTCTCTCCACTATAATTTGTACAATGCA 900
  |||||
  301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
  |||||
  901 TCTAATAGCGGTGTTTATATGATATGAGAAATATTTTAATGGTTCGT 950
  |||||
  317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
  |||||
  951 GGTGCAAAACATCCACACATCGCGTTACTTTTGTTCACAATGTTTAAAC 1000
  |||||
  334 exGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
  |||||
  1001 CTCAGCCCGGGGAGCATTTGGAATCCTTTGTTCACAATGTTTAAACCA 1050
  |||||
  351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
  |||||
  1051 CTTGATATGCAATGGTTCGTGACAGGGGACAAAGTTTATCCTCCGTATT 1100
  |||||
  367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
  |||||
  1101 TTATGGGATTTACTACGGTATCCCAACCCATGGTTCGGCTATGAAAT 1150
  |||||
  384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
  |||||
  1151 CTAATAATAGACCCCTCTTCTGACAGGCACGTCAAACTTTTGCCTATGTC 1200
  |||||

```

```

401 GlnHisAspTyrPheAspHisHisAspIleGlyTrpThrArgGluG1 417
|||||
1201 CAGCATGATTACTTGGATCATCATGATATATCGTTGGACAAGAGGG 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGCTCCCATCCAAATTCAGGCGCTGCCACCATATATGCAGATGGTC 1300
|||||
434 roGlyGlyAsnLysTyrMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGTTACAAATGGATGATGTGGGGAATAAAGCGGACAGATT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATTACCGGAATAGGACAGGCGCCGCACAAATTAATGCAGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
|||||
1401 CGGATGGGGTAATTTCTCTTAATGGAGGTCGGTTTCGGTTTGGGTGA 1450
|||||
484 ySgln 485
|||||
1451 AGCAA 1455

```

seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:us-09-170-670-9

```

seq_documentation_block:
; Sequence 9, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170, 670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063, 306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-9

```

```

alignment_scores:
Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

```

alignment\_block:

US-09-590-375-2 x US-09-170-670-9 ..

Align seg 1/1 to: US-09-170-670-9 from: 1 to: 1455

```

1 H1HisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCATATGGAACAAATGCTACTATCATCATATATTCGAATGGTATT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAsnL 34
|||||
51 GCCAAATGACGGGAATCATTTGGAAACAGGTTGAGGGATGACGCACTAACT 100
|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||
101 TAAAGAGTAAGGATTAACAGCTGTATGGATCCCACTGATGGAAGGG 150
|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuGlu 67
|||||

```

```

151 ACTTCCAGAAATGATGTAGTTATATGGCCCTATCATTTATATGATCTGG 200
|||||
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGGGGAGCTTCGTACAAAATATGGAACACGCAACC 250
|||||
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGCTGGGTGACCTCTTTAAAAAATAACGGCATTCAGTATAT 300
|||||
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCGTATGAATCATAAAGGTGGAGCAGATGGTACGGAATGT 350
|||||
117 LAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134
|||||
351 AAATGCGGTAGAGTGAATCGGAGCAACCGAAACCCAGGAACCTCAGGAG 400
|||||
134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAGCGTGGACAAAGTTTGTATTTCTCGAAGAGGAAT 450
|||||
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTCAGCTTAAAGTGGCGCTGTATCATTTTGTATGGACAGATTG 500
|||||
167 PAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
|||||
184 LysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGGCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGTATGACAGCGTGGATATGGATCACCAGAGTAATATACATGAAC 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTGGGGAGTGGGTATAGCAATACACTGAACTTGTATGGATTATA 700
|||||
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGCAGTGAACATATAAATATAGCTTTACGAGAGATTGGCTT 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGCGTAACACCACAGGTAAACCAATGTTTGCAGTGGCTGAGTT 800
|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGGAATAATGACCTTGGTGAATTTGAAACTATTTGAATAAAACAAGTT 850
|||||
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCACTCGGTGTTGATGTTCTCTCCACTATATTTGTACAAATGCA 900
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGTTATATGATATGAGAAATATTTTAAATGGTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTCAAAAACATCCACACATGCCGTACTTTTGTGATAACCATGAT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAGCCCGGGAGAGCATTTGGAATCCTTTGTTCAACAAATGGTTAAACCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||

```

```

1051 CTGCATATGTCATGGTCTTGTACAAAGGAACAAGTTATCTTCCTCGTATT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
1101 TTATGGGGATTACTACGGTATPCCCAACCCATGGGTTCGGGCTATGAAT 1150
384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
1151 CTAATATAGACCTCTCTCGAGCAGCAGTCAAACTTTTGGCTATGGTACG 1200
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGI 417
1201 CAGCATGATTACTTTGTATCATCATGATATATATCGGTTGGACAGAGAGGG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1251 AAATAGCTCCCATCAAAATCAGGCGCTTGGCCACCATTATGTCAGATGGTC 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1301 CAGGTGGTAACAAATGGATGTATGTGGGAAAAATAAAGCGGGACAAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1351 TGGAGAGATATTACCGGAAATAGACAGCCACCGTCACAAATTAATGCGAGA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTyrValL 484
1401 CGGATGGGTAAATTCCTGTCTTAATGGAGGTCGCTTCGGTTGGGTGA 1450
484 ysGln 485
1451 AGCAA 1455

```

seq\_name: /cgn2\_6/ptodata/2/ina/68\_COMB.seq:US-09-170-670-14

# seq\_documentation\_block:

```

; Sequence 14, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-14

```

## alignment\_scores:

```

Quality: 2613.00      Length: 485
Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381      Percent Identity: 95.052

```

## alignment\_block:

```

US-09-590-375-2 x US-09-170-670-14
Align seg 1/1 to: US-09-170-670-14 from: 1 to: 1455
1 HisHisAsnGlyThrAsnGlyThrMetGlnTyrPheGluTrpHisLe 17
1 CATCATATGGAAACAATGGTACTATGATGATCAATATTCGAATGCTATT 50

```

```

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGATGACGAGTAAC 100
34 eUysSerLysGlyIleThrAlaValTrpIleProAlaTyrLysGly 50
101 TAAAGAGTAAAGGATAACAGCTGTATGGATCCACCTGCATGGAGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeu 67
151 ACTTCCAGAAATGATGATGAGTTATGGAGCCTCATGATTTATGATCT 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSer 84
201 AGAGTTTAAACCAAGAGGGGACGCTTCGTACAAAATATGGAACACG 250
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnVal 100
251 AGCTACAGGTGCGGTGACCTCTTTAAAAAATAACGGCATTCAGGTAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMet 117
301 GGTGATGTCGTCATCAATCAATAAGGTGGACGAGTGGTACGGAAAT 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluLysSerG 134
351 AAATCGGTAGTAGTGAATCGGAGCAACCGAAACAGGAAACCTCAGG 400
134 lutyThrIleGluAlaThrLysPheAspPheProGlyArgGlyAsn 150
401 AGTATCAATAGAAAGCGTGGACAAGTTTGAATTTCTTGGAGAGGAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAs 167
451 AACCATTCACGCTTAAAGTGGCGTGGTATCATTTTGTATGGGACAG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyTh 184
501 GGATCAGTCACGCCAGCTTCAAAAACAAAATATATAAATTCAGGGGA 550
184 lYlysAlaTyrAspTrpGluValAsnGlyAsnGlyAsnTyrAspTyr 200
551 GCAAGGCTGGGACTGGGAATCGATACAGAGAATGGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGl 217
601 CTTATGATGCAGACGTGGATATGGATCACCACAGAAGTAATACATA 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyP 234
651 TAGAACTGGGGAGTGGTATACGAATACACTGAACCTTGATGGATT 700
234 rGileAspAlaValIysHisIleLysTyrSerTyrThrArgAspTrp 250
701 GAATAGATGCAGTCAACATATAAATATAGCTTTACGAGAGATTGGCT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGl 267
751 ACACATGTGCGTAAACACACAGGTAACCAATGTTTGCAGTGGCTGAG 800
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrS 284
801 TTGGAAAAATGACCTTGGTGCATGGAATGAAAACATATTGTAATAA 850
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsn 300
851 GGAATCACTCGGTGTTTGTATGTTCTCTCCACTATAAATTTGTACA 900
301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
901 TCTAATAGCGGTGTTTATATGATATGAGAAATATTTTAAATGGTCT 950

```



```
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTGCAAAACATCCACACATGCCGTACTTTTGTGTGATAACCATGATT 1000

334 erGlnProGlyGluAlaLeuGlnSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTGAGCCCGGGGAGCAATGGAAATCCCTTTGTTCAACAATGGTTTAAACCA 1050

351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTGTCATATGCATGGTCTGCACAGGGAACAAGTTATCTTCCGTATT 1100

367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 TTATGGGATTAATACGGTATCCCAACCCATGGTGTTCGGCTATGAAT 1150

384 erLysIleAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAATAAGACCCCTCTCTCGAGCAGCTCAAACTTTTGGCTATGGTACG 1200

401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrThrArgGluG 417
|||||
1201 CAGCATGATTACTTTGATCATCATGATATATCGGTGGACAGAGAGG 1250

417 yAspSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGCTCCCATCCAAATTCAGGCCCTTGCACCATTTATGTCAGATGTC 1300

434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGGTAACAATGATGATGTGTGGGAAAAATAAAGCGGACAAAGTT 1350

451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATTACCGGAATATAGGACAGGACCGTCACATTTAATGCAGA 1400

467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
|||||
1401 CGGATGGGTAAATTTCTCTGTTAATGAGGTCGTTTCGGTTTGGGTGA 1450

484 ysGln 485
|||||
1451 AGCAA 1455
```

seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:us-09-193-068-9

seq\_documentation\_block:

; Sequence 9, Application US/09193088.

; Patent No. 6197565

; GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan

; APPLICANT: Kjrulff, S ren

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Andersen, Carsten

; TITLE OF INVENTION: -Amylase Variants

; FILE REFERENCE: 5709.000-US

; CURRENT APPLICATION NUMBER: US/09/193,068

; CURRENT FILING DATE: 1998-11-16

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 9

; TYPE: DNA

; ORGANISM: Bacillus sp.

US-09-193-068-9

alignment\_scores:

Quality: 2613.00

Ratio: 5.421

Percent Similarity: 99.381

Percent Identity: 95.052

alignment\_block:

Length: 485

Gaps: 0

```
US-09-590-375-2 x US-09-193-068-9
Align seq 1/1 to: US-09-193-068-9 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCATATATGGAACAATGGTACTATGATGATCAATATTTTCAATGGTATT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
|||||
51 GCCAATACAGCGGAATCATTTGGACAGGTTGAGGATGACGACGCTAACT 100

34 eulysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
|||||
101 TAAAGACTAAAGGATAACAGCTGTATGGATCCACCTGCATGGAAGGG 150

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
|||||
151 ACTTCCAGAAATGATGTAGGTTATGGAGCCTATGATTTATATGATCTTGG 200

67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACACAGAGGGGACGGTTCGTACAAAATATGGAACACGCAAC 250

84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGCTGGGTGACCTCTTTAAAAAATAACGCGCATTCAGGTATAT 300

101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATCTCGTCATGAATCATAAAGGTGGAGCAGATGTTACGGAAATGT 350

117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGlnIleSerGlyG 134
|||||
351 AAATCGCGTAGAGTGAATCGGAGCAACCCAAAACAGCAACCTCAGAG 400

134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAAGCGTGGACAAAGTTTGTATTTCTCTGGAAGAGAAAT 450

151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTTCCAGCTTTAAGTGGCGCTGGTATCATTTTGTGGACAGATTG 500

167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCAGCCAGCTTCAAAACAANAATATATAAATTCAGGGGAACAG 550

184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGGCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600

201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGTATGCAGACGTGGATGATGATCACCAGAGTAATACATGAACT 650

217 uATGAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTGGGAGTGGGTATACGAATACACTGAACCTTGTATGGATTTA 700

234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGCAGTGAACATATATAAATATAGCTTTACGAGAGATTGGCTT 750

251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGGTAACACACACAGGTAAACCAATGTTTGCAGTGGCTGAGTT 800

267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGAAAAAATGACCTTGGTCAATTTGAAACTATTTTGAATAAAACAAGTT 850

284 rAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
```

us-09-590-375-2.rni

Thu Nov 29 10:43:47 2001

```
|||||
851 GGAATCACTCGGTGTTGATGTTCTCTCCACATATATTTGTACAAATGCA 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGTTATATGATATGAGAAATATTTAAATGGTCTGCT 950
317 lvalGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTGCAAAACATCCACACATGCGGTACTTTGTTGATACCATGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCACCCCGGGAGCAGTGGATGCTTTGTTCAACAATGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGlnGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCATATGCAATGTTCTGACAAGGGAACAAGGTTATCCTCCGTATT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 TTATGGGGATTACTACGGTATCCCAACCCATGGTGTTCGGCTATGAAT 1150
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrClyThr 400
|||||
1151 CTAATAATAGACCTCTCTCTGACGGCACGTCAAAACTTTGGCCTATGGTACG 1200
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGlu 417
|||||
1201 CAGCATGATTACTTGGATCATCATGATATATTCGGTTGACAAAGAGAGG 1250
417 YaspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGTCCCATCCAAATTCAGGCTTCCACCATATGTGAGATGGTC 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGTACAAATGATGATGTGTGGGAAATAAAGCGGACAAAT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGATATATTCGGAAATAGGACAGGACCGTCACAAATTAATGCAGA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
|||||
1401 CGGATGGGTAAATTTCTCTTATGAGGTCGGTTTCGGTTGGGTGA 1450
484 ysGln 485
|||||
1451 AGCAA 1455
```

seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:us-09-193-068-13

```
seq_documentation_block:
; Sequence 13, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kirulff, S ren
; APPLICANT: Bisgaard-Prantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-193-068-13
```

```
alignment_scores:
Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052
alignment_block:
US-09-590-375-2 x US-09-193-068-13
Align seg 1/1 to: US-09-193-068-13 from: 1 to: 1455
1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCATATGGAACAAATGGTACTATGATGCAATATTTGGAATGGTATT 50
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
|||||
51 GCCTAATGACGGGAATCATTTGGAACAGGTTGAGGGATGCGCAGCTAAT 100
34 eulysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||
101 TAAAGAGTAAAGGATAACAGCTGTATGATCCACCTGCATGGAGGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeu 67
|||||
151 ACTTCCAGAAATGATGATGATGATGAGGCTATGATTTATATGATCTTG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGGAGGAGCGTTCGTACAAATATGGAACACGCAAC 250
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGTGCGGTGACCTCTTTAAAAAATAACGCGCATTCAGGTAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCGTATGATGATGATGATGATGATGATGATGATGATGATG 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134
|||||
351 AAATGCGGTAGAGTGAATCGGACCAACCCGAAACCCAGCAACCTCAGG 400
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAACGCTGGACAAGTTTGATTTCTCTGGAAGAGGAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpThrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTCCAGCTTTAAGTGGCGCTGGTATCATTTTGTGAGGACAGATT 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
184 lLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGCCCTGGGACTGGGAAGTCGATACAGAGATGGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGATGCAGACGCTGGATATGGATCACCAGAAAGTAATACATGAAT 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAACCTGGGAGTGTGTTATACGGAATACATGAACTTGTATGATT 700
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGCAGTGAACATATAAATATAGCTTACGAGAGATTGCTT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
```

```
751 ACACATGTGCGTAACACACAGTAAACCAATGTTTGCAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
|||||.....|
801 TTGGAANAATGACCTGGTGGCAATTCGAACACTATTTGAATAAACCAAGTT 850
284 rPasnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||.....|
851 GGAATCACCTCGGTGTTGTATGTTCTCTCCACATATAATTGTTACATGCA 900
301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
901 TCTAATAGCGGTGGTATTATGATGATGAGAAATATTTAAATGGTCTGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
951 GGTGCAANAACATCCACACATGCCGTGTACTTTGTTGATAACCAATGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
1001 CTCAGCCCGGGGAAGCATTTGGAATCTTGTTCACAAATGGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
1051 CTTGCATATGCATTTGTTCTGCAAGGGAACAAGGTTATCTCTCCGTATT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
1101 TTATGGGGATTACTACGGTATCCCAACCCATGGTGTCCGGCTATGAAT 1150
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
1151 CTAATAATAGACCTCTTCTCGCAGGCAGTCAAACTTTTGCTATGTGTACG 1200
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrThrArgGlu 417
1201 CACCATGATTACTTTGATCATCATGATATATATCGTTGGACAAGAGAGG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1251 AATAGCTCCCATCCAAATTCAGCCCTTGCACCAATATGTCAGATGGTC 1300
434 rGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1301 CAGGTGGTAACAAATGATGTATGTGGGAAAAATAAAGCGGCACAAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1351 TGGAGAGATATTACCGGAATAGGACAGGCACCGTCACAATTAATGCAGA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
1401 CGGATGGGTAAATTTCTCTGTTAATGGAGGGTCGGTTTCGGTTGGGTGA 1450
484 ysGln 485
|||||
1451 AGCAA 1455
```

seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: us-09-183-412-9

```
seq_documentation_block:
; Sequence 9, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
```

```
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus
US-09-183-412-9

alignment_scores:
Quality: 2613.00      Length: 485
Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:
US-09-590-375-2 x US-09-183-412-9 ..

Align seg 1/1 to: US-09-183-412-9 from: 1 to: 1455

1 H1SH1SAsnGlyThrAsnGlyThrMetGlnTyrPheGluTrpHisLe 17
|||||.....|
1 CATCATAAATGGAACAAATGCTACTATGATGCAATATTTTGAATGGTATT 50
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
|||||.....|
51 GCCAATGACGGGAATCATTTGGAAACAGGTTGAGGGATGACGCACTAACT 100
34 eUlySerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||.....|
101 TAAAGAGTAAAGGATAACAGCTGTATGGATCCACCTGCATGGAAGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTrpLeuG 67
|||||.....|
151 ACTTCCAGAAATGATGTAGGTTATGGAGCCTATGATTTATATGATCTTG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSer 84
|||||.....|
201 AGAGTTTAAACCAAGGGGACGGTTCGTACAAAATATGGACACGCAACC 250
84 lNLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||.....|
251 AGCTACAGGTCGGGTGACCTCTTTAAAAAATAACGGCATTTCAGGTATAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||.....|
301 GGTGATGTCGTCATGAATCATAAAGGTGGAGCAGATGTTACGGAAATGT 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134
|||||.....|
351 AATGCGGTAGAAGTGAATCGGAGCAACCCAAACCAAGAACTCAGAG 400
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||.....|
401 AGTATGCAATAGAAGCGTGACAAAAGTTTGTATTTCTCGTGAAGAGAAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||.....|
451 AACCATTCACGCTTAAAGTGGCGCTGCTATCATTTTGTATGGACAGATTG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||.....|
501 GGATCAGTCAGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAC 550
184 lYlYsAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
```

```
|||||
551 GCAAGGCTGGGACTGGGAGCTGCATACAGAGAATGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
601 CTTATGATGACAGCGTGGATATGGATGATCCACAGAGTAATACATGAAT 650
217 uArgAspTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
651 TAGAACTGGGAGTGGTATACGATACATACACTGAACCTTGATGGATTGA 700
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
701 GAATAGATGCAGTGAACATATAAATATAGCTTTACGAGAGATTGGCTT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
751 ACACATGTGCTTAACACACAGGTAACCAATGTTGAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
801 TTGAAAAATGACCTTGGTGAATTGAAACTATTGTAATAAACAAAGTT 850
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
851 GGAATCACTCGGTGTTGATGTTCTCTCCACTATAATTGTACAATGCA 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
901 TCTATACGGTGGTATTATGATATGATATGAGAAATATTTAAATGGTCTGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
951 GGTGCAAAACATCAACACATCGCGTTACTTTGTTGATAACCATGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
1001 CTCAGCCGGGAGAGCATGGTAATCTTTGTCAACAATGGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
1051 CTGCAATATGATGGTCTGCACAGGGAACAAGGTTATCTCCGTATT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
1101 TTATGGGATTACTACGGTATCCCAACCCATCGTGTCCGCTATGAAAT 1150
384 erLysIleAspProLeuLeuGlnAlaAtgGlnThrTyrAlaTyrGlyThr 400
1151 CTAAATAGACCTCTCTGAGGACAGCTCAACCTTTGCCCTATGGTACG 1200
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417
1201 CAGCATGATTACTTTGATCATCATCATATATATCGGTTGGACAAGAGGG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1251 AAATAGCTCCCATCAATTCAGGCTTGCCCAACCATTTATGTCAGATGGTC 1300
434 rGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1301 CAGGTGGTAACAAATGGATGATGTGGGGAATAATAAGCGGACAAAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1351 TGGAGAGATATTACCGGAATAGGACAGCCGTCACAAATTAATGTCAGA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
1401 CGGATGGGGTAATTTCTCTGTAAATGGAGGGTCCGTTTCGGTTGGGTGA 1450
484 ysGln 485
|||||
```

```
1451 AGCAA 1455
seq_name: /cgn_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-13
seq_documentation_block:
; Sequence I3, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Garsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-183-412-13

alignment_scores:
Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:
US-09-590-375-2 x US-09-183-412-13 ..
Align seg 1/1 to: US-09-183-412-13 from: 1 to: 1455
1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
1 CATCATATGGACAAATGGTACTATGATGCAATATTTTCGAATGCTATTT 50
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
51 GCCAAATGACGGGAATCATTTGACACAGTTGAGGATGACCCAGCTAACT 100
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
101 TAAAGAGTAAAGGGATAACAGCTGTATGGATCCCACTGCATGGAAGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
151 ACTTCCCAGAAATGATGATAGGTATGAGGCCCTATGATTTATATGATCTGG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
201 AGAGTTTAAACCAAGAGGAGCGGTTCGTACAAAATATGGAACACGCAACC 250
84 inLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
251 AGCTACAGGCTCGGTGACCTCTTTAAAAAATAACGCAATTCAGGTATAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
301 GGTGATGTCGTCATGATCAATAAAGGTGGAGCATGGTACGGAATTTGT 350
```

```
117 lAsnAlaValIcLuValAsnArgSerAsnArgAsnGlnGlnIleSerGlyG 134
|||||
351 AAATGCGGTAGAAGTGAATCGGAGCAACCGAAACCGAACCTCAGGAG 400
|||||
134 luYrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAAGCGTGACAAAGTTTGAATTTCTGGAAGAGGAAT 450
|||||
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACATTCACGCTTAAAGTGGCGCTGTATCATTTTGTATGGGACAGATTG 500
|||||
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACGCGCAGCTTCAAAACAAATATATAAATTCAGGGGAACAG 550
|||||
184 lYlYsAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGGCGTGGGAGTGGGAAGTCGATACAGAGAAATGGAACACTATGACTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGTATGCACAGCTGGGATATGGATCACCCAGAGTATATACATGAAC 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTGGGGAGTGGGTATACGAATACACATGAACTTTGATGGATTATA 700
|||||
234 rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGAGTGAACATATATAAATATAGCTTTACGAGAGATTGGCTT 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGGGTACACACAGCAGTAACCAATGTTTGCAGTGGCTGAGTT 800
|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
|||||
801 TTGCAAAATGACCTTGGTGCAATTTGAAACTATTTCAATAAAACAAGTT 850
|||||
284 rPasnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCACTCGGTGTTGATGTTCTCTCCACTATAATTTGTACAATGCA 900
|||||
301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGGTATTATGATATGAGAAATATTTTAATGCTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTGCAAAACATCCACACATGCGGTACTTTGTTGATAACCATGATT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAGCCGGGGAGCAGTGAATCCCTTGTTCACCAATGGTTTAAACCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCATATGCATGGTCTCGACAGGGAACAAGTTATCTCTCCGTATT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 TTAGGGGATTACTACGCTATCCCAACCCATGGTGTCCGCTATGAAT 1150
|||||
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAATAATAGACCTCTTTCGAGGACGCTCAAACTTTTGCTATGGTACG 1200
|||||
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl 417
|||||
1201 CAGCATGATTAATTTGATCATCATGATATATATCGTTGGACAAGAGAGG 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
```

```
|||||
1251 AAATAGCTCCCATCCAAATTCAGGCTTGCACCATTTATGTCAGATGTC 1300
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGTAACAAATGATGTATGTGGGAAAAATAAGCGGCAAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGACATATTACCGAAATAGGACAGGACCGCTCACATTAATATGAGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
|||||
1401 CGGATGGGTAAATTTCTGTGTAATGAGGCGTCGTTTCGTTTGGGTGA 1450
|||||
484 ySGln 485
|||||
1451 AGCAA 1455
|||||

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-354-191A-4

seq_documentation_block:
; Sequence 4, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-354-191A-4
```

```
alignment_scores:
  Quality: 2613.00      Length: 485
  Ratio: 5.421          Gaps: 0
  Percent Similarity: 99.381  Percent Identity: 95.052

alignment_block:
US-09-590-375-2 x US-09-354-191A-4
```

Align seg 1/1 to: US-09-354-191A-4 from: 1 to: 1455

```
1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
1 CATATAATGCAACAAATGGTACTATGATGCAATATTTTCGAATGGTATT 50
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
51 GCCAAATGACGGGAATCATTCGACAGAGTTGAGGATGACCGACTACT 100
34 euLysSerLysGlyThrAlaValTrpIleProProAlaTrpLysGly 50
101 TAAGAGTAAAGGATAACACCTGTATGATGCCACCTGCATGGAAGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTrpAspLeuValTrp 67
151 ACTTCCCAAGATGATGAGTATGAGCCCTATGATTTATATGATCTTGG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
201 AGAGTTTAAACAGAGGAGCGTTCGTCAAAATATGGAACACCGCAACC 250
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTrp 100
251 AGCTACAGCTCGCGTACCTCTTTAAAAAATAACGGCATTACAGGTATAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
301 GGTGATGTCGTATCAATCAATAAAGGTGGAGAGATGTCGGAATTTGT 350
117 IAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluLysSerGly 134
351 AAATCGGTAGAGTGAATCGGAGCAACCGAAACCCAGGAAACCTCAGGAG 400
134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
401 AGTATGCAATAGAACGCTGGACAAATTTGATTTCTTGGAAAGAGAAAT 450
151 ThrHisSerAsnAspPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
451 AACCATTCAGCTTTAAGTGGCGCTGGTATCATTTTGGGACAGATG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
501 GGATCAGTCACGCCAGCTTCAAAACAAATATATAAATTCAGGGGAACAG 550
184 IyLysAlaTrpAspTrpGluValAspIleGluAsnGlyValAsnTyrAspTyr 200
551 GCAAGCCCTGGGACTGGGAAGTCGATACAGAAATGGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
601 CTTATGATGACAGCTGGTATGATGATCACCAGAAAGTAATACATGAAC 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
651 TAGAACTGGGAGTGGTATACGAATACACTGAACCTTGATGGATTTA 700
234 rGileAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
701 GAATAGATGAGTGAACATATATAAATATAGCTTTACGAGAGATTGGCTT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
751 ACACATGTCGTTAACACACAGGTAACCAATGTTTGCAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
801 TTGGAAAAATGACCTTGGTGAATTCGAACTATTTTGAATAAACAGTT 850
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
```

```
851 GGAATCACTCGGTGTTTGATGTTCTCTCCACTATATAATTTGTACAATGCA 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
901 TCTAATACCGGTGGTATTATGATATGAGAAATATTTTAATGGTCTGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
951 GGTGCAAAAAACATCCAACACATGCCGTACTTTTGTGTGATAAACCATGTT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
1001 CTCAGCCCGGGAGCATTCGATCTTTTGTCAACAATGGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
1051 CTTCATATGCAATGGTCTCTGACAAAGGAAACAGGTTATCCTTCCTGATT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
1101 TTATGGGATTTACTACGTATCTCCCAACCCATGGTGTTCGGCTATGAAT 1150
384 erLysIleAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
1151 CTAATATAGACCTCTCTCGACGACGCTCAAACTTTTGCTATGGTACG 1200
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417
1201 CAGCATGATTTACTTTGATCATCATGATATATTCGTTGGACAAGAGAGG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1251 AAAATAGTCCCATCCAAATCAGGCTTGCACCATTATGTCAGATGTC 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1301 CAGGTGGTAACAAATGGATGATGTGGGGAATAAAGCGGACAAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1351 TGGAGATATTTACCGAAATAGGACAGGACCGCTCACAATTAATGTCAGA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
1401 CGGATGGGTAAATTTCTCTGTTAATGAGGTCCTCGTTTCGGTTGGGTGA 1450
484 ysGln 485
1451 AGCAA 1455
```

seq\_name: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:us-08-600-908A-11

```
seq_documentation_block:
; Sequence 11, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394,204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1458 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1455
; US-08-600-908A-11

```

## alignment\_scores:

```

Quality: 2613.00      Length: 485
Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

```

## alignment\_block:

```
US-09-590-375-2 x US-08-600-908A-11 ..
```

```
Align seg 1/1 to: US-08-600-908A-11 from: 1 to: 1458
```

```

1 HisHisAsnGlyThrAsnGlyThrMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCATAAATGGAACAAATGTTACTATGATGCAATATTCGAATGGTATTT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
|||||
51 GCCAAATGACGGGAAATCTTGGAAACAGGTTGAGGGATGACGCAGCTAACT 100
|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
|||||
101 TAAAGAGCTAAAGGATAACAGCTGTATGGATCCACCTGCATGGAAGGGG 150
|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuGlu 67
|||||
151 ACTTCCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 200
|||||
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACAGAGAGGGGACGGTTCGTACAAAATATGGAAACCCCAACC 250
|||||
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGCTGCGGTGACCTCTTTAAAAAATAACGCCATTCAGGTATAT 300
|||||
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGCTGCTAATGAAATATAAGGTGGAGCAGATGTTACGGAAATTTG 350
|||||
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGlnLysSerGlyG 134
|||||
351 AAATGCGGTAGAGTGAATCGGAGCAACCCGAAACCCAGGAACCTCAGAG 400
|||||
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAACCGCTGGACAAAGTTGATTTCTCTGGAAGAGGAAT 450
|||||
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTTCCAGCTTTAAGTGGCGCTGTATCATTTTGTATGGAGAGATTTG 500

```

```

167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThr 184
|||||
501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
|||||
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGGCCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGATGACAGCTGGGATATGGATCACCAGAACTAATACATGAACT 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTGGGGAGTGGTATACGAATACACTGAACCTTGATGGATTAA 700
|||||
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGCAGTGAACATATAAAATATAGCTTTACGAGAGATTTGGCTT 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGCGTAACACACAGGTAAACCAATGTTGCAGTGGCTGAGTT 800
|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
|||||
801 TTGGAAAAATGACCTTGGTGAATTTGAAAACCTATTTGAATAAAAACAGTT 850
|||||
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCAGCTCGGTGTTGATGTTCTCTCCACTATAATTTGTACAATGCA 900
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGTTTATGATGATGATGAGAAATATTTTAAATGTTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTCAAAACACATCCACACATGCGGTACTTTTGTGATAAACCATGATT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAGCCCGGGAAGCATTTGGAATCCTTTGTTCAACAATGTTTAAACCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCATATGCATTGGTTCGACAGGGAACAAGGTTATCCTTCGGTATT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 TTATGGGGATTACTACGGTATCCCAACCCATGGTTCGGCTATGAAT 1150
|||||
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAAATAGACCCCTCTTCGACGACGTCAAACTTTTTCCTATGTTGTTACG 1200
|||||
401 GlnHisAspTyrPheAspHisHisAspIleGlyTrpThrArgGluCl 417
|||||
1201 CAGCATGATTACTTTGATCATCATGATATATCGGTTGGCAAGAGAGGG 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGTCCCTCCAAATTCAGGCCCTTCGCCCATTTATGTTCAGATGGTC 1300
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGTGGTTACAAAATGATGATGTTGCGGAAAAATAAAGCGGGACAAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGATATATTACCGGAAATAGGACAGGCCCGCTCACAATTAATGTCAGA 1400

```

467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
 1401 CGGATGGGGTAATTCCTCTGTTAATGAGGGTCCGTTTCGGTTGGGTGA 1450

484 ysGln 485  
 1451 AGCAA 1455

seq\_name: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:us-08-683-838A-11

seq\_documentation\_block:  
 ; Sequence 11, Application US/08683838A  
 ; Patent No. 6022724  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Bisg rd-Frantzen, Henrik  
 ; APPLICANT: Borchert, Torben Vedel  
 ; TITLE OF INVENTION: -Amylase Mutants  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSSEE: NO. 6022724O NO. 6022724disk of No. 6022724th America, Inc.  
 ; STREET: 405 Lexington Avenue, 64th Floor  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: United States of America  
 ; ZIP: 10174-6401  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/683,838A  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/600,908  
 ; FILING DATE: 13-FEB-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Green, Reza  
 ; REGISTRATION NUMBER: 38,475  
 ; REFERENCE/DOCKET NUMBER: 4394.204-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-867-0123  
 ; TELEFAX: 212-878-9655  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1458 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..1455  
 ; US-08-683-838A-11

alignment\_scores:  
 Quality: 2613.00 Length: 485  
 Ratio: 5.421 Gaps: 0  
 Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:  
 US-09-590-375-2 x US-08-683-838A-11

Align seg 1/1 to: US-08-683-838A-11 from: 1 to: 1458

1 HisHisAsnGlyThrAsnGlyThrMetGlnTrpPheGluTrpHisLe 17  
 1 CATCATATGGAACAAATGGTACTATGATGCAATATTTTCAATGGTATT 50  
 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34

51 GCCAATGACGGGAATCARTGGAACAGGTTGAGGATGACGACGTAAC 100  
 34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50  
 101 TAAAGAGTAAAGGATACAGCTGTATGATCCACCTGCATGGAAGGG 150  
 51 ThrSerGlnAsnAspValGlyTyrGlyAlaValTrpAspLeuGly 67  
 151 ACTTCCAGAAATGATAGTTATGAGGCTATGATTTATATGATCTGG 200  
 67 YGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
 201 AGAGTTTAAACAGAGGGGACGGTTCGTACAAAATATGGAACACGCAACC 250  
 84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
 251 AGCTACAGGCTCGGTGACCTCTTTAAAAAATAACGGCATTCAGGTATAT 300  
 101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
 301 GGTGATCTCTCATGAATCATAAAGGTGGACAGATGGTACGGAATTTGT 350  
 117 LAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
 351 AAATCGGTTAGAGTGAATCGGACCAACCCAGAACCCAGAACCTCAGGAG 400  
 134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
 401 AGTATGCAATAGAACGCTGGACAAAGTTTGATTTCTCTGGAAGAGGAAAT 450  
 151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
 451 AACCATTCACAGCTTTAAGTGGCGCTGGTATCATTTTGTATGGACAGATTG 500  
 167 PAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
 501 GGATCAGTCACGCCAGCTTCAAAAACAAAATATATAAATTCAGGGGAACAG 550  
 184 IlyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
 551 GCAGGCTGGGACTGGGAAGTCGATACAGAGATGGCAACTATGACTAT 600  
 201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
 601 CTATATGATGCAGAGCTGGATATGATCACCAGAAAGTAATACATGAACT 650  
 217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
 651 TAGAACTGGGAGTGTGTATACGAATACACTGAACCTTGATGGATTGA 700  
 234 rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
 701 GAATAGATCCAGTGAACACATATAAATAATAGCTTTACGAGAGATTGGCTT 750  
 251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
 751 ACACATGTGCTAACCAACACAGCTAACCAATGTTTTCAGTGGCTGAGTT 800  
 267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSert 284  
 801 TTGGAATAATGACCTTGGTGCATTTGAAACATATTTTGAATAAACAAAGTT 850  
 284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
 851 GGAATCACCTCGGTGTTTGTATGTTCTCTCCACTATATAATTTGTACAATGCA 900  
 301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
 901 TCTAATAGCGGTGTTTATATGATATGAGAAATATTTTAAATGGTCTGT 950  
 317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334



```

951 GGTGCAAAACATCCACACATCGCGTTACTTTGTTGATAACCATGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
1001 CTCACCCCGGGAGCATGGTAATCTTTGTTCAACAATGGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuLeuLeuThrArgGluGlnGlyTyrProSerValPh 367
1051 CTTGCATATGCAATGGTCTGACAAAGGGAACAAGTTATCCCTCCGTATT 1100
367 eYrGlyAspTyrTyrGlyLeuProThrHisGlyValProSerMetLysS 384
1101 TTATGGGGATTACTACGGTATCCCAACCATGGTGTTCGGGTATGAAT 1150
384 erLysileAspProLeuLeuGlnAlaAtrGlnThrTyrAlaTyrGlyThr 400
1151 CTAAATAGACCCCTCTTCGAGGACGCTCAAACTTTGCTTATGGTAGC 1200
401 GlnHisAspTyrPheAspHisHisAspIleLeuGlyTyrThrArgGluG 417
1201 CAGCATGATTACTTTCATCATCATGATATATCGGTTGGACAAGAGGG 1250
417 yAspSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1251 AAATAGCTCCCATCCAAATTCAGGCTTTCGCCACCATTTATGTCAGATG 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1301 CAGGTGGTAACAAATGGATGATGTGGGGGAAAAATAACCGGACAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1351 TGGAGAGATATTACCGGAAATAGGACAGCCGTCACACATTAATGCACA 1400
467 pGlyTrpGlyAsnPherValAsnGlyAlaValSerValTrpValL 484
1401 CGGATGGGTAATTTCTCTGTTTAATGGAGGTCCTTCGTTTGGGTGA 1450
484 ysGln 485
1451 AGCAA 1455

```

seq\_name: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:US-08-446-803-5

```

seq_documentation_block:
; Sequence 5, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Otrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rabbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCE: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESS: No. 5824531 No. 5824531disk of No. 5824531th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.803
; FILING DATE: 01-June-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.

```

```

; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-446-803-5

alignment_scores:
    Quality: 2440.00      Length: 485
    Ratio: 5.148          Gaps: 0
    Percent Similarity: 97.732    Percent Identity: 86.598

alignment_block:
US-09-590-375-2 x US-08-446-803-5
Align seg 1/1 to: US-08-446-803-5 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
1 CATCAATATGGGACAAATGGGACGATGATGCAATCTTTGAATGGCATT 50
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
51 GCCTAATGATGGGAATCACATCGAATAGATTAGAGATGATGCTAGTAATC 100
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
101 TAAGAAATAGAGGTATTAACCGCTATTATTGGATTCCCGCTCCCTGGAAGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
151 ACTTCGCAAAATGATGTGGGTATGGAGCTATGATCTTTATGATTTAGG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
201 GGAATTTAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGCTAGTC 250
84 InLeuGlnGlyAlaValThrSerLeuLysAsnGlyIleGlnValTyr 100
251 AATTGGAGTCTGCCATCCATCTTTAAAGAAATAATGGCGTTCAAGTTAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
301 GGGGATGTAGTATGATGAACCAATAAAGGAGGAGCTGATGCTACAGAAACGT 350
117 lasnAlaValGluValAsnArgSerSerAsnArgAsnGlnGluIleSerGlyG 134
351 TCTTGTCTGCGAGGTGAATCCAAATCAACCGGAATCAAGAAATATCTCGGG 400
134 luTyrThrIleGluAlaTyrThrLysPheAspPheProGlyArgGlyAsn 150
401 ACTACACAATTTGAGGCTTGACTTAAGTTTTCAGGAGGGGTAAT 450
151 ThrHisAsnPhelystTrpArgTrpTyrHisPheAspGlyThrAspTr 167
451 ACATACCTCAGACTTTAAATGGCGTTTGGTATCATTTTCGATGGTGTAGATTG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
501 GGATCAATCAGCAATTCCAAAATCGTATCTACAAATTCGAGAGGTGATG 550
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlnLysAsnTyrAspTyr 200
551 GTAAGGCATGGGATTGGGAAGTAGATTTCGGAATAATGGAATTTATGATTAT 600

```

```

201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 TTAATGATCCAGATGTAGATATGGATCATCCGGAGGTAGTAAATGAGCT 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAGATGGGAGAAATGGTATACAAATACATTAATCTTGATGGATTTA 700
|||||
234 rgIleAspAlaValLysHisIleIleIleIleIleIleIleIleIle 250
|||||
701 GGATCGATGGGTGAGCATATTAATATATAGCTTTACACGTGATGGTTG 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACCATGTAGAACAACGCAACGGGAAAGAATGTTTCTGCTGCTGAATT 800
|||||
267 eTrpLysAsnAspLeuAlaIleIleGluAsnTyrLeuAsnLysThrSert 284
|||||
801 TTGGAAAAATGATTTAGTGCTGCTTGGAGAACTATTTAAATAAACAAC 850
|||||
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCATCTGCTTGTATGATGCTCCCTTCATTTATATCTTTTAAACGC 900
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCAATAGTGGAGGCAACTATGACATGGCAAACTTCTTAATGGAACGGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 TGTTCAAAAGCATCAATGATGCGGTAACTTTTGTGGATTAATCACGATT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCACCTGGGGAATCATTAAGATCTTTTACAAAGATGCTTTAAAGCCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTGTGTTATGCGCTTATTTTAAAGAGAAAGGCTATCCCTCTGTCTT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 CTATGCTGACTACTATGGAATCCAAACATAGTGTCCAGCAATGAAG 1150
|||||
384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CCAAGATTGATCCAACTTAGAGCGCGTCAAAATTTTGCATATGGAACA 1200
|||||
401 GlnHisAspTyrPheAspHisAspIleIleGlyTrpThrArgGluG1 417
|||||
1201 CAACATGATTATTTTGACCATCAATAATAATCGGATGACACAGTGAAG 1250
|||||
417 yAspSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATACAGCATCCCAATTCAGGACTTCGACTATCATGTCGGATGGC 1300
|||||
434 roGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGGGGAGAGAAATGGATGTACGTAGGCGCAAAATAAAGCAGGTCAAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGATGACATTAACGTGGAATAAATACAGGAAACAGTACGATCAATGCAGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
|||||
1401 TGGATGGCTAATTTTTCAGTAAATGGAGGATCTGTTCATTTGGGTGA 1450
|||||
484 ysGln 485
|||||
1451 AACGA 1455

```

seq\_name: /cgn2\_6/ptodata/2/1na/5B\_COMB.seq:US-08-861-837-5

```

seq_documentation_block:
; Sequence 5, Application US/08861837
; Patent No. 5856164
; GENERAL INFORMATION:
; APPLICANT: Ottup, Helle
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Bacillus Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5856164o No. 5856164disk of No. 5856164th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861.837
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446.803
; FILING DATE: 01-June-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 4157.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-861-837-5

```

```

alignment_scores:
Quality: 2440.00 Length: 485
Ratio: 5.148 Gaps: 0
Percent Similarity: 97.732 Percent Identity: 86.598

alignment_block:
US-09-590-375-2 x US-08-861-837-5 ..
Align seg 1/1 to: US-08-861-837-5 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCAATAATGGCAAAATGGACCATGATGATCACTTTGAATGACACTT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAsnL 34
|||||
51 GCCTAATCATGGAAATCACTGGAATAGATTAAAGATGATGCTAGTAATC 100
|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||
101 TAAGAAATAGAGGTATAACCGCTATTTGATTCGCCCTGCCTGGAAGGG 150
|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG1 67
|||||
151 ACTTCGCAAAATGATGCTGGGTATGGACCTATGATCTTTATGATTAGG 200
|||||

```

```
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 GGAATTAAATCAAAAGGGGACGCTCGTACTAAGTATGGACACGTAATC 250
84 InLeuGlnGlyAlaValThrSerLeuLysAsnGlnGlyLeuValTyr 100
|||||
251 AATTGGAGTCTGCCATCCATCGCTTTAAAGAAATAATGGCGTTCAAGTTAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGGATGTAGTATGATGACCAATAAGGAGGAGCTGATGCTACAGAAACGT 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351 TCTTGCTGTCGAGGTGAATCCAAATCAACCGAATCAAGAAATATCTGGGG 400
134 luTyrThrIleGluAlaThrPheLysPheAspPheProGlyArgGlyAsn 150
|||||
401 ACTACACAATTTGAGGCTTGAGCTTAAGTTTTCAGGGAGGGGTAAT 450
151 ThrHisSerAsnPhelLysTrpArgTyrHisPheAspGlyThrAspTr 167
|||||
451 ACATCTCAGACTTTAAATGGCGTTGGTATCATTTTCGATGGTATGATG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAATCAGCAATTCCTCAAAATCGTATCTACAAATTCAGAGTCAATG 550
184 lYlAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GTAAGGCATGGGATGGGAAGTAGATTCGGGAAATGGAATATGATGATAT 600
201 LeuMetTrpAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 TTAATGTATCCAGATGATAGATATGGATATCCGGAGGTAGTAATAGACT 650
217 uArgAsnTrpGlyValTyrThrAsnTrpLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAGATGGGAGATGGTATACAAATACATTAATCTTGATGGATTTA 700
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GGATCGATGGCGTGAAGCATATTAAATATATAGCTTTACACGCTGATGGT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACCCATGTAAAGAACCGCAACGGGAAGAAATGTTGCTGTTGCTGAAT 800
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGAAAAATGATTAGTGCCTTGGAGAACTATTAAATAAACAACAACT 850
284 rAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCATCTGCTTGTATGTCCTCCCTTCATTATATATCTTTTATAACGC 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCAATAGTGGAGCAACTATGATGATGCGAAACTTCTTAATGGAACGGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 TGTTCAAAACATCCATGATGATGCGTAACTTTTGTGATAATACAGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAACCTGGGGATCAATAGATCATTTTGTACAAGAAATGGTTTAAGCCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCTTATCGCTTATTTTAAAGAGAAACAAGGCTATCCCTCTGTCCT 1100
```

```
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 CTATGGTACTACTATGTAATTCACACATAGTGTCCACAGCAATGAAG 1150
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CCAAGATTTGATCCAAATCTTAGAGCGCGTCAAAATTTTGCATATGAACA 1200
401 GlnHisAspTyrPheAspHisHisAspIleGlyTrpThrArgGluG 417
|||||
1201 CAACATGATTATTTTACCATCATATAATTCGATGGACACGTGAAGG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATACCACGCATCCCAATTCAGGACTTGCAGCTATCATCTCGATGGGC 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGGGAGAGAAATGGATGATGCTAGCTAGGCAAAATAAGCAGGTCAA 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGCATGACATAACTGGAATAAACAGGAACAGTTACGATCATGCGAGA 1400
467 pGlyTrpGlyAsnPhetrValAsnGlyGlyAlaValSerValTrpVal 484
|||||
1401 TGGATGGCTAATTTTTCAGTAAATGGAGGATCTGTTTCCATTGGGTGA 1450
484 ysgln 485
|||||
1451 AAGCA 1455

seq_name: /cgn2_6/ptodata/2/ina/6a_COMB.seq:us-08-600-656-5

seq_documentation_block:
; Sequence 5, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Prantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562ch America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,656
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

US-08-600-656-5

## alignment\_scores:

Quality: 2440.00 Length: 485  
Ratio: 5.148 Gaps: 0  
Percent Similarity: 97.732 Percent Identity: 86.598

## alignment\_block:

US-09-590-375-2 x US-08-600-656-5 ..

Align seg 1/1 to: US-08-600-656-5 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTyrHisLe 17  
|||||  
1 CATATAATGGGACAAATGGGACGATGATGCAATACCTTGAATGGCACTT 50  
|||||  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAsnL 34  
|||||  
51 GCCTAATGATGGAACTACTGGAATAGATTAAGAGATGATGCTAGTATC 100  
|||||  
34 euLysSerLysGlyThrAlaValTrpIleProAlaTrpLysGly 50  
|||||  
101 TAAGAAATAGAGGTATAACCGCTATTTGGATTCCCGCTGCCCTGGAAAGG 150  
|||||  
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuGly 67  
|||||  
151 ACTTCGCAAAATGATGTGGGTATGGAGCCATGATGATCTTTATGATTAGG 200  
|||||  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
|||||  
201 GGAATTTAATCAAAAGGGGACGGTTCCGTACTAAGTATGGGACACGATGC 250  
|||||  
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
|||||  
251 AATTGGAGTCTCCATCCATGCTTTAAAGAAATAATGGCGTTCAAGTTTAT 300  
|||||  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||  
301 GGGGATGTAGTGAACCATAAAGGAGGAGCTGATGCTACAGAAAAGCT 350  
|||||  
117 IAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
| | | | |  
351 TCTTGCTGTCGAGGTGAATCCAAATCAACCGGAATCAAGAAATATCTGGGG 400  
| | | | |  
134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
| | | | |  
401 ACTACACAAATTCAGGCTTGGACTAAGTTTGATTTCCAGGGAGGGTAAT 450  
| | | | |  
151 ThrHisSerAsnPhelystTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
| | | | |  
451 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTTCGATGGTGTAGATTG 500  
| | | | |  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
| | | | |  
501 GGATCAATCAGACAAATCCAAATCGTATCTACAAATTCGAGGTGATG 550  
| | | | |  
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
| | | | |  
551 GTAAGGCATGGGATTGGGAAGTAGATTCGGAATAATGGAATATGATTAT 600  
| | | | |  
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
| | | | |  
601 TTAATGTATGCAGATAGATATGGATATCCCGAGGTAGTAATAGAGCT 650  
| | | | |  
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
| | | | |  
651 TAGAAGATGGGAGATGGTATACAAATACATTAATCTTGATGGATTTA 700  
| | | | |  
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
| | | | |  
701 GGATCGATGGGTGAAGCATATTAATAATATAGCTTTTACACGTGATTGGTTG 750



1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluThrPheHisLe 17  
|||||  
238 CATCATATATGGACGACGATGGGACCATGATGACGATATTTTGAATGGCATTT 287  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34  
|||||  
288 GCCAAATGACGGGAACCACTGGAACAGGTAGCAGATGACGACGAGCTAACT 337  
34 euLysSerLysGlyLeuThrAlaValTrpIleProProAlaTrpLysGly 50  
|||||  
338 TAAAGAGTAAAGGGATTACCGCTGTTTGGATTCCCTCCATCGGAAGGG 387  
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67  
|||||  
388 ACTTCGCAAAATGATCTTGGGTATGCTGCTATGATTTGTACGATCTTGG 437  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
|||||  
438 TGAAGTTTAAACCAAGGGAACCGTCCGTCGTAACAAATATGCCAAGGAGTC 487  
84 lnteuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
|||||  
488 AGTTGCAAGTCCGCTGACATCTTTGAAAAATAACGGGATTCAGGTTTAT 537  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||  
538 GGGCATGCTGATGAATCATAAAGGTGGACGACAGCGGACAGAGATGTT 587  
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
|||||  
588 AAATGGCGTGGAAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTG 637  
134 lutyThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
|||||  
638 AATACACCATTTGAAGCATGGACGAAATTTGATTTCCCTGGACAGGAAAT 687  
151 ThrHisSerAsnPhelysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
|||||  
688 ACCCATTTCCAACTTTAAATGGCGCTGGTATCATTTTGTGGGACAGATTG 737  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
|||||  
738 GGATCAGTCACGTCAGCTTCAGAACAAATATATATAATTCAGAGGTACCG 787  
184 lLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
|||||  
788 GAAAGGCATGGGACTGGGAAGTAGATAGATAGAGAACGCGCAACTATGATTAC 837  
201 LeuMetTyrAlaAspIleAspMetAspHisProGlnValIleAsnGluLe 217  
|||||  
838 CTTATGTATGCAGACATGTGATATGGATCATCCAGAGTAATATCAATGAACT 887  
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
|||||  
888 TAGAAATGGGAGTTTGGTATACAAATACACTTAATCTAGATGGATTTA 937  
234 rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
|||||  
938 GAATCGATGCTGTGAAACATATTAAATACAGCTATACGAGAGATTGGCTA 987  
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
|||||  
988 ACACATGTGGTACACACACAGGTAAACCAATGTTTCAGTTGCAGAAAT 1037  
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
|||||  
1038 TTGAAAAATGACCTTGTCTGCAATCGAAACCTATTTAAATAAAACAAGTT 1087  
284 rAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
|||||  
1088 GGAATCACTCGCTTGCATGTTCTCTTCATATATAATTTGTACAAATGCA 1137  
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlyServa 317

|||||  
1138 TCTAATAGTGTGGCTATTTTGTATGATGAGAAATATTTTAAATGGTCTCTGT 1187  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334  
|||||  
1188 CGTCAAAAACACCCCTATACATGACGAGTCACATTTGTTGATTAACCATGACT 1237  
334 eGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
|||||  
1238 CTCACCCAGGAGAGCAATTTGGAATCCTTTGTTCAATCGTGGTTCAACCA 1287  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
|||||  
1288 CTGGCATATGCATTTGATCTGCAAGGAGCAAGGTTACCCCTTCCTGATTT 1337  
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384  
|||||  
1338 TTACGCTGATTACTACGGTATATACCAACTCATGTGTTCTCTCGATGAAAT 1387  
384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
|||||  
1388 CTAAATTTGATCCACTTCTGACGACGCTCAAACTGATGCTCGCTACGGAACC 1437  
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrThrArgGluG 417  
|||||  
1438 CAACATGATTATTTGATCATCATCATATATATCGCTGGACGAGAGAAGG 1487  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
|||||  
1488 GCACAGCTCCCAACCAATTCAGGACTTGCAACTATTTATGTCGATGGGC 1537  
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
|||||  
1538 CAGGGGTAAATAATGATGATGTCGGGAAACATAAAGCTGCCCAAGTA 1587  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
|||||  
1588 TGGAGAGATATCACCGAAATAGGTCTGTGCTACCGTCACCATTAATGCAGA 1637  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
1638 TGTTGGGGAAATTTCACTGTAAACGAGGGGCAGTTTCGTTTGGGTGA 1687  
484 ySgln 485  
|||||  
1688 AGCAA 1692  
seq\_name: /SID52/gcdata/geneseq/geneseq/NA2000.DAT: AAC66234  
seq\_documentation\_block:  
ID AAC66234 standard; DNA; 1786 Bp.  
XX  
AC AAC66234;  
XX  
DT 19-FEB-2001 (first entry)  
XX  
DE Mutant alpha-amylase nucleotide sequence.  
XX  
KW Alpha-amylase; detergent; Bacillus; ds.  
XX  
OS Bacillus sp.  
XX  
PN JP20000245466-A.  
XX  
PD 12-SEP-2000.  
XX  
PF 25-FEB-1999; 99JP-0048213.  
XX  
PR 25-FEB-1999; 99JP-0048213.  
XX  
PA (KAOS ) KAO CORP.  
XX  
DR WPI; 2000-615143/59.

DR P-PSDB: AAB35714.  
 XX A novel mutant alpha-amylase for use in a detergent composition -  
 XX  
 XX Example 1; Page 6-9; 12pp; Japanese.  
 XX  
 CC The present invention relates to a mutant alpha-amylase. Included in the  
 CC invention are a gene encoding the mutant alpha-amylase, a vector  
 CC containing the gene, and a transformed cell recombined by the vector. The  
 CC enzyme is used in a detergent composition. The present sequence  
 CC represents the mutant alpha-amylase gene.  
 XX  
 SQ Sequence 1786 BP; 578 A; 307 C; 420 G; 481 T; 0 other;

alignment\_scores:  
 Quality: 2713.00 Length: 485  
 Ratio: 5.594 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000  
 alignment\_block:  
 US-09-590-375-2 x AAC66234 ..  
 Align seg 1/1 to: AAC66234 from: 1 to: 1786  
 1 HisHisAsnGlyThrAsnGlyThrMetGlnTyrPheGluTrpHisLe 17  
 |||||  
 248 CATCATATGGGACCAATGGGACCATGATGCAGTATTTGAATGCAATT 297  
 |||||  
 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAsnL 34  
 |||||  
 298 GCCAATGACGGGACCACTGGACAGGTACGAGATGACGCACTAACT 347  
 |||||  
 34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50  
 |||||  
 348 TAAAGAGTAAGGGGATACCGCTGTTGGATTCCTTCCTGCAATGGAAGGG 397  
 |||||  
 51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67  
 |||||  
 398 ACTTCGCAAAATGATGTTGGGTATGGTGCCTATGATTGTTAGCATCTGG 447  
 |||||  
 67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
 |||||  
 448 TGAGTTTAAACCAAGGAAGGACCGTCCTGACAAAATATGCGCAAGAGTC 497  
 |||||  
 84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
 |||||  
 498 AGTTGCAAGGTGCGGTGCATCTTTGAAAATTAACGGGATTCACGTTTAT 547  
 |||||  
 101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
 |||||  
 548 GGGGATGTCGTGATCAATCATAAAGGTGGAGCAGACGGGACAGATGGT 597  
 |||||  
 117 IasnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
 |||||  
 598 AAATCGGTGGAGGTGAACCGGAACCAACGAAACCAAGAAATATATCAGGTG 647  
 |||||  
 134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
 |||||  
 648 AATACACCATTTGAACATGAGGACGAAATTTGATTTCCCTGGAAGAGGAAAT 597  
 |||||  
 151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
 |||||  
 698 ACCCATTCCAACTTTAAATGGCGCTGGTATCATCTTTGATGGGACAGATTG 747  
 |||||  
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
 |||||  
 748 GGATCAGTCACGTCAGCTTCAGACAAAATATATAAATTCAGAGGTACCG 797  
 |||||  
 184 lYLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
 |||||  
 798 GAAAGGCATGGGACCTGGGAAGTAGATATAGAGAACGCAACTATGATTAC 847  
 |||||

201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
 |||||  
 848 CTTATGTATGCAGACATTTGATATGATCATCCAGAAGTAATCAATGAAC 897  
 |||||  
 217 uArgAsnTrpGlyValTyrTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
 |||||  
 898 TAGAAATTTGGGAGTTTGGTATACAAAACACTTAATCTAGATGATTTA 947  
 |||||  
 234 tGileAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
 |||||  
 948 GAATCGATGCTGTGAACATATTAATACAGCTATACGAGATGGCTA 997  
 |||||  
 251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
 |||||  
 998 ACACATGTGCGTAAACACACAGGTAAACCAATGTTTGCAGTTGCAGAAT 1047  
 |||||  
 267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
 |||||  
 1048 TTGGAAAAATGACCTTGTGCAATCGAAACACTATTTAAATAAAACAAGTT 1097  
 |||||  
 284 tPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
 |||||  
 1098 GGAATCACTCCGTTCGATGTTCTCTTCATTATTAATTTGTACAAATGCA 1147  
 |||||  
 301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
 |||||  
 1148 TCTAATAGTGGTGGCTATTTGATATGAGAAATATTTAAATGGTCTCTGT 1197  
 |||||  
 317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334  
 |||||  
 1198 CGTACAAAACACCTTATACATGCAGTCACATTTGTTGATAACCATGACT 1247  
 |||||  
 334 exGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
 |||||  
 1248 CTCAGCCAGGAGAACGATGGAAATCTTTGTTCAATCGTGGTTCAACCA 1297  
 |||||  
 351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
 |||||  
 1298 CTGGCATATGCATTGATTTCTGACAAAGGAGCAAGGTTACCCCTTCGGTATT 1347  
 |||||  
 367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384  
 |||||  
 1348 TTACCGGTGATTACTACGGTATACCAACTCATGGTGTCTCCTTCGATGAAAT 1397  
 |||||  
 384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
 |||||  
 1398 CTFAAATTTGATCCACTTCTGCAGGACGCTCAAACTGATGCTTACGGAACC 1447  
 |||||  
 401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrThrArgGluG 417  
 |||||  
 1448 CAACATGATTTATTTTGATCATCATGATATATCGGCTGGACGAGAGAGG 1497  
 |||||  
 417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
 |||||  
 1498 GGACAGCTCCCAACCAAAATTCAGAGCTTGCAACTATTATGTCCGATGGGC 1547  
 |||||  
 434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
 |||||  
 1548 CAGGGGGTAAATAAATGGATGATGTGCGGAAACATAAAGCTGGCCCAAGTA 1597  
 |||||  
 451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
 |||||  
 1598 TGGAGAGATATCACCGGAAATAGGTCTGTGTCGTCACCATTAATATGAGA 1647  
 |||||  
 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484  
 |||||  
 1648 TGGTTTGGGGGAATTTCACTGTAAACGGAGGGGACGTTTGGGTTGGGTGA 1697  
 |||||  
 484 ysGln 485  
 |||||  
 1698 AGCAA 1702

seq\_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT: AAT00776

```

seq_documentation_block:
ID   AAT00776 standard; DNA; 1455 BP.
XX
AC   AAT00776;
XX
DT   16-MAR-1996 (first entry)
XX
DE   Bacillus sp. alkaline alpha-amylase DNA.
XX
KW   Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile;
KW   beer; starch; ss.
XX
OS   Bacillus.
XX
PN   W09526397-A1.
XX
PD   05-OCT-1995.
XX
PF   29-MAR-1995; 95WO-DK00142.
XX
PR   03-FEB-1995; 95DK-0000123.
PR   29-MAR-1994; 94DK-0000353.
PR   03-NOV-1994; 94DK-0001271.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Bisgard-frantzen H, Ostergaard PR, Outtrup H, Rasmussen MD;
PI   Van DER ZEE P;
XX
DR   WPI: 1995-351318/45.
DR   P-PSDB; AAR81835.
XX
PT   New alkaline Bacillus alpha-amylase - used in e.g. detergent
PT   compsns. starch liquefaction, textile desizing, starch modification
PT   or beer making
XX
PS   Disclosure; Page 48-49; 65pp; English.
XX
CC   This DNA sequence may be expressed recombinantly for the production
CC   of an alpha-amylase protein. The produced protein is characterized
CC   by having a specific activity at least 25% higher than the specific
CC   activity of Termamyl at 25-55 deg C and a pH of 8-10. The enzyme
CC   can be used in detergent composition for starch liquefaction, the
CC   production of lignocellulosic materials, e.g. pulp, paper and
CC   cardboard from waste containing starch, for deinking recycled
CC   starch-coated, or starch- containing printed paper, to modify
CC   starch for papermaking, for textile desizing, and beer-making
CC   processes.
XX
SQ   Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

```

```

alignment_scores:
Quality: 2613.00      Length: 485
Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052

alignment_block:
US-09-590-375-2 x AAT00776 ..
Align seg 1/1 to: AAT00776 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CAFCATAATGGACAAATGGTACTATGATGCAATATTCGAATGGTATT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
|||||
51 GCCAAATAGCGGAATCATTTGGACAGGTTGAGGATGACGCGTAAC 100
|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||

```

```

101 TAAAGACTAAAGGATAACAGCTCTATGGATCCACCTGCATGGAAGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG1 67
|||||
151 ACTTCCAGAAATGATGAGGTTATGGAGCCTATGATTTATATGATCTGG 200
67 YGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGGGGACGCTTCGTACAAAATATGGAACACCAACC 250
84 InLeuGlnGlyAlaValThrSerLeuLysAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGTCGCGTGACCTCTTTAAAAAATAACGCAATTCAGGTATAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCGTGATGATCAATAAGGTGGAGCAGATGGTACGGAATTTGT 350
117 IAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351 AAATGCGGTAGAGTGAATCGGAGCAACCGAAACACAGGAACCTCAGGAG 400
134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATCAATAGAACGCTGGACAAAGTTTGATTTCTCTGGAAGAGAAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTCAGCTTTAAGTGGCGCTGGTATCATTTTGATGGGACAGATTG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACGCCAGCTTCAAAACAAATAATATAAAATTCAGGGGAACAG 550
184 LysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGCCCTGGGACTGGGAGTCGATACAGAGAAATGGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGATGACAGCTGGATGATGATGATCACCAGAAAGTAATACATCACT 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTGGGAGTGTGTATACGAATACACTGAACCTTGATGGATTTA 700
234 rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATCAGTGAACATATAAATATAGCTTTTACGAGAGATTGGCTT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTCGTAAACACACACAGGTAACCAATGTTTGCAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGGAAAAATGACCTGGTGCATTTGAAACACTATTITGAATAAAACAAGTT 850
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCAGCTCGGTGTTGATGTTCTCTCCACTATAAATTTGTACAAATGCA 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGGTTATTATGATATAGAAAATATTTTAAATGGTTCGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334
|||||
951 GTGCAAAAACATCCACACACATGCCGCTTACTTTTGTGATAACCATGATT 1000
334 eGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAGCCCGGGAGCATTTGGAATCCTTTGTTCAACAATGGTTTAAACCA 1050

```



351 LeuAlaTyrAlaLeuLeuLeuThrArgGluGlnGlyTyrProSerValph 367  
 1051 CTTGCATATGATGGTTCTGCACAAGGAACAAGTTATCTTCGCTATT 1100  
 367 eYrGlyAspTyrTyrGlyLeuProThrHisGlyValProSerMetLys 384  
 1101 TTTATGGGGATTTACTACGGTATCCCAACCCATGGTGTTCGCGCTATGAAT 1150  
 384 eYrLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
 1151 CTAATAATAGACCTCTCTCAGGACGCTCAACTTTTGCTATGGTACG 1200  
 401 GlnHisAspTyrPheAspHisHisAspIleleGlyTyrThrArgGlu 417  
 1201 CAGCATGATTACTTTGATCATCATGATATTATCGTTGGACAAGAGAGG 1250  
 417 YAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGly 434  
 1251 AAATAGTCCCATCTCAAAATTCAGGCCCTTGCCACCATTTATGTCAGATGGTC 1300  
 434 roGlyGlyAsnLysTyrMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
 1301 CAGGTGTACAAATGGTGTATGTGGGAAAATAAAGCGGCAAGTT 1350  
 451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
 1351 TGGAGAGATATTACCGAAATAGGACAGCCAGCCGTCACAAATTAATGCGA 1400  
 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484  
 1401 CGGATGGGGTAATTTCTCTGTTAATGGAGGGTCGGTTTCGGTTGGGTGA 1450  
 484 ysGln 485  
 1451 AGCAA 1455

seq\_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAx59632

seq\_documentation\_block:

ID AAX59632 standard; DNA; 1455 BP.

XX AC AAX59632;

XX DT 22-JUL-1999 (first entry)

XX DE DNA encoding a termamyl-like alpha-amylase protein.

XX KW Termamyl-like; alpha-amylase; variant; washing; dishwashing;  
 KW production; sweetener; ethanol; starch; textile desizing;  
 KW starch liquefaction; saccharification process; ss.

XX OS Bacillus sp.

XX PN WO9923211-A1.

XX PD 14-MAY-1999.

XX PF 30-OCT-1998; 98WO-DK00471.

XX PR 14-JUL-1998; 98DK-0000936.

XX PR 30-OCT-1997; 97DK-0001240.

XX PA (NOVO ) NOVO-NORDISK AS.

XX PI Andersen C, Borchert TV, Kjaeruliff S, Nielsen BR;

XX PI Nissen TL, Svendsen A;

XX DR WPI; 1999-326987/27.

XX DR New Termamyl-like alpha-amylase variants

XX PT Disclosure; Page 91-92; 115pp; English.

XX PS

XX

The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present sequence encodes an amylase that can function as the parent sequence in the production of the variants of the invention.

XX Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment\_scores:

Quality: 2613.00 Length: 485  
 Ratio: 5.421 Gaps: 0  
 Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AAX59632 ..

Align seg 1/1 to: AAX59632 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
 1 CATCATATGGAAACAAATGGTACTATGATGCAATATTTTCGAATGGTATT 50  
 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34  
 51 GCCAAATGACGGGAATCATTTGGAAACAGTTGAGGGATGACCGACTAACT 100  
 34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50  
 101 TAAAGAGTAAAGGATAACAGCTGTATGGATCCACCTGCATGGAAGGG 150  
 51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeu 67  
 151 ACTTCCAGATGATGATGAGTTATGGAGCCCTATGATTTATATGATCTGG 200  
 67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSer 84  
 201 AGATTTTAAACCAAGGGGACGGTTCGTACAAATATGGAACACGCAACC 250  
 84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
 251 AGCTACAGGCTCGGTGACCTCTTTAAAAAATAACGGCATTTCAGGTATAT 300  
 101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
 301 GGTGATGTCGTGATGAATCATATAAGGTGGAGCAGATGTTACGAAATTTG 350  
 117 IAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134  
 351 AAATCGGTTAGAGTGAATCGGACCAACCGAAACCAACCAACCTCAGAG 400  
 134 IuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
 401 AGTATGCAATAGAACGCTGGACAAAGTTTGATTTTCTGGAAGAGGAAT 450  
 151 ThrHisSerAsnPheLysTrpArgTyrTrpHisPheAspGlyThrAspTr 167  
 451 AACCATTCAGCTTTAAAGTGGCGTGTGATCATTTTGTATGGACAGATTG 500  
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThr 184  
 501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550

```
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGCCTGGGACTGGGAAGTCATACAGAAATGGCAACTATGACTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGTATGCAGACGTGGATATGGATATGATGATGATGATGATGATG 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTGGGAGTGTGTATACGATACACTGAACCTTGATGATTTA 700
|||||
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATCAGTGAACATATATAAATATAGCTTTACGAGAGATGGCTT 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGCGTAACACACAGGTAAACCAATGTTTGCAGTGGCTGAGTT 800
|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGGAATAATGACCTTGGTGCAATCTGAAACATATTTGAAATAAACAA 850
|||||
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCAGTCGGTGTGATGTTCCCTCCACTATAAATTTGTACATGCA 900
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGTATATATGATATGACAAATATTTTAAATGGTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsp 334
|||||
951 GGTGCAAAAACATCCAAACATGCGCTTACTTTGTGTGATACCATGATT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAGCCCGGGAGCATGGAAATCTTTGTTCAACAATGGTTTAAACCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGlnGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCATATGCATGTTGTTCTGCAAGGGAACAAGTTATCTTCGTATT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 TTATGGGGATTACTACGATATCCCAACCATGGTGTTCGGCTATGAAT 1150
|||||
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAATAATAGACCTCTTCTGCAGGCACGTCAACTTTTGCCTATGGTAG 1200
|||||
401 GlnHisAspTyrPheAspHisAspIleIleGlyTrpThrArgGluGl 417
|||||
1201 CAGCATGATTACTTTGATCATCATATATATATATATATATATATATAT 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGCTCCCATCAAAATTCAGGCTTGGCCACCATATATGTCAGATGTC 1300
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisIleGlyGlnVal 450
|||||
1301 CAGGTGGTAAACAAATGGATGATGATGGGAAAAAATAAGCGGACAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATTACCGAAATAGGACGACCGTCACAATTAATGTCAGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
|||||
1401 CGATGGGGTAATTTCTCTGTAAATGGAGGGTCCGTTTCGGGTTGGGTGA 1450
|||||
484 ysGln 485
```

|||||

1451 AGCAA 1455

seq\_name: /SIDS2/gcgdata/geneseq/NA1999.DAT:AA59636

seq\_documentation\_block:

ID AAX59636 standard; DNA; 1455 BP.

XX AAX59636;

XX 22-JUL-1999 (first entry)

XX DNA encoding a termamyl-like alpha-amylase protein.

DE Termamyl-like; alpha-amylase; variant; washing; dishwashing;  
KW production; sweetener; ethanol; starch; textile desizing;  
KW starch liquefaction; saccharification process; ss.

OS Bacillus sp.

XX WO9923211-A1.

PD 14-MAY-1999.

XX 30-OCT-1998; 98WO-DK00471.

XX 14-JUL-1998; 98DK-0000936.

PR 30-OCT-1997; 97DK-0001240.

XX (NOVO ) NOVO-NORDISK AS.

XX Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;

PI Nissen TL, Svendsen A;

XX WPI; 1999-326987/27.

XX New Termamyl-like alpha-amylase variants

XX Disclosure; Page 98; 115pp; English.

XX The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275, K311, E346, K385, G456, N457, K459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present sequence encodes an amylase that can function as the parent sequence in the production of the variants of the invention.

XX Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment\_scores:

Quality: 2613.00 Length: 485

Ratio: 5.421 Gaps: 0

Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AAX59636 ..

Align seg 1/1 to: AAX59636 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17

|||||

1 CATCATATGGAACAAATGGTACTATGATGCAATATTTGCAATGATATT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34

```

|||||
51 GCCAAATGACGGGATCATTTGGAACAGGTTGAGGATGACGACGCTAACT 100
|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||
101 TAAAGAGTAAAGGATAACAGCTGTATGGATGCCACCTGCATGGAAGGG 150
|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG1 67
|||||
151 ACTTCCCAAGATGATGATAGGTTATGGAGCCTATGATTTATATGATCTGG 200
|||||
67 yLupPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGAGGAGGCTTCGTACAAAAATATGGAACACGCAACC 250
|||||
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGCGTGGGTGACCTCTTTTAAAAAATAACGGCATTCAGGTATAT 300
|||||
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCGTATGAATCATATAAGGTGGACAGATGCTACGGAATGTGT 350
|||||
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351 AAATGCGGTAGAAGTGAATCGGACGCAACCGAAACAGGAAACCTCAGGAG 400
|||||
134 luTyrThrIleGluAlaThrPheLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAAGCTGGACAAAGTTTGATTTTCTTGGGAAGAGAAAT 450
|||||
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTCAGCTTTAAGTGGCGTGGTATCATTTTGTATGGACAGATTG 500
|||||
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCAGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
|||||
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGCGCTGGAGCTGGGAAGTCGTACAGAGATGGCAACTATGACTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGTATGCAGAGCTGGATATGGATCACCAGAAATATACATGAAC 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAACTGGGAGTGTGGTATACGAATACACGTGAACCTTGATGGATT 700
|||||
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGAGTGAACACATATAAATATAGCTTTACGAGAGATTGGCT 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGCGTAAACACACAGGTAACCAATGTTTGCAGTGGCTGAGTT 800
|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGGAAAAATGACCTTGTGTGCAATTAATAAATATTTGTAATAAACAAGTT 850
|||||
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCACTCGGTGTTGATGTCTCTCCACTATAATTTGTAACAAATGCA 900
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTANTAGCGGTGTTATATGATATGAGAAATATTTAAATGGTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||

```

```

951 GGTGCAAAAAACATCCACACATGCGCTTACTTTTGTGATAACCATGATT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCACCCCGGGAAGCATTTGGAATCCTTTGTTCAACAATGGTTTAAACCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTTGTCATATGCATTGTTCTGACAAGGAACAAGCTTATCCTTCGCTATT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
|||||
1101 TTATGGGATTACTAGCTATCCCAACCCATGCTTCCGGCTATCAAT 1150
|||||
384 erLysIleAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAAATAGACCTCTTCTGAGGACACGTCAAAACCTTTGCCCTATGGTACG 1200
|||||
401 GlnHisAspTyrPheAspHisHisAspIleLeGlyTyrThrArgGluG1 417
|||||
1201 CAGCATGATTACTTTGATCATCATGATATATCGGTTGGACAAGAGAGG 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGTCCCATCCAAATTCAGGCTTCCACCATTTATGTCAGATGGTC 1300
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGGTAACAAATGGATGTATGTGGGAAATAAAGCGGACAAAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGACAGATATTACCGGAAATAGGACAGCACGCGTCACAATTAATGCAGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
|||||
1401 CGGATGGGTAAATTTCTCTGTTAATGGAGGTCGCTTTCGGTTTGGGTGA 1450
|||||
484 ysGln 485
|||||
1451 AGCAA 1455

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAx57597
seq_documentation_block:
ID AAX57597 standard; DNA; 1455 BP.
XX
AC AAX57597;
XX
DT 16-JUL-1999 (first entry)
XX
DE Wild type Termamyl(RTM)-like alpha-amylase coding sequence #6.
XX
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction;
KW sweetener; ethanol; ss.
XX
OS Bacillus sp.
XX
PN W09919467-A1.
XX
PD 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK00444.
XX
PR 13-OCT-1997; 97DK-0001172.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Bisgard-Frantzen H, Borchert TV, Svendsen A;
XX
DR WPI; 1999-277632/23.
XX

```

PT Variant alpha-amylases - useful as detergents or for textile  
 PT desizing or starch liquefaction  
 XX  
 PS Disclosure; Page 83-84; 93pp; English.  
 XX

CC This sequence represents the coding sequence for a parent sequence  
 CC used to generate new variants of a termamyl-like alpha-amylase with  
 CC alpha-amylase activity. The variants comprise mutations in 2-6  
 CC regions/positions relative to an alpha-amylase from either of two  
 CC Bacillus species in W09526397, B. stearothermophilus, B. licheniformis,  
 CC B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants  
 CC are amyloglucosidases or amylomannanases used for dishwashing, manual  
 CC or automatic laundry. The variants can also be used for textile desizing  
 CC or starch liquefaction (e.g. for production of sweeteners or ethanol).  
 XX

SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment\_scores:  
 Quality: 2613.00 Length: 485  
 Ratio: 5.421 Gaps: 0  
 Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:  
 US-09-590-375-2 x AAX57597 ..

Align seg 1/1 to: AAX57597 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
 1 CATCATATGGAACAAATGGTACTATGATGCAATATTTCCGAATGGTATT 50  
 17 uproAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34  
 51 GCCAAATGACGGGAATCAATGGACAGGTGGAGGATGACCACTACT 100  
 34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50  
 101 TAAAGAGTAAAGGGATAACAGCTGTATGATCCACCTGCATGGAAGGG 150  
 51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuGlu 67  
 151 ACTTCCCAAGATGATGATGATGAGCCATGATGATTTATATGATGATGG 200  
 67 ygluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerg 84  
 201 AGAGTTTAAACAGAGGGGCGGTTCGTACAAAATATGGAACACGCAACC 250  
 84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGluValTyr 100  
 251 AGCTACAGCTCGGTGACCTCTTTTAAAAAATAACGGCATTCAGGTATAT 300  
 101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
 301 GGTGATGTCGTATGAATCATAAAGGTGGAGCAGATGTCGGAATGT 350  
 117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
 351 AAATCGGTGAGAGTGAATCGGAGCAACGGAACAGGAACCTCAGGAG 400  
 134 lutyThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
 401 AGTATCAATAGAAGCGTGGCAAGATTTGATTTTCCCTGGAAGAGAAAT 450  
 151 ThrHisSerAsnPhelysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
 451 AACCATCCAGCTTTAAGTGGCGCTGATCATTTTGTATGGGACAGATTG 500  
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
 501 GGATCAGTCACGCGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550  
 184 lLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200

551 GCARGCCCTGGAGCTGGAGCTGCATACAGAGAAATGGCAACTATCACTAT 600  
 201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
 601 CTTATGTATGAGAGCTGGATGATGATCACCAGAAATGATACATGAAT 650  
 217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
 651 TAGAACTGGGAGCTGGTATACAAATACACTGAACCTTGATGATTAT 700  
 234 rGileAspAlaValLysHisLysTyrSerTyrThrArgAspTrpLeu 250  
 701 GAATAGATGACAGTGAACATATAAATATAGCTTACGAGAGATGGCTT 750  
 251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
 751 ACACATGTCGCTAACACACACAGGTAAACCAATGTTGCAGTGGCTGAGT 800  
 267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284  
 801 TTGGAAAATGACCTTGGTGCATTTGAAAACCTATTTGAATAAAACAGT 850  
 284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
 851 GGAATCAGCTCGGTGTTGATGTTCTCTCCACTATAATTTGACAAATGCA 900  
 301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
 901 TCTAATAGCGGTGGTATTATGATATGAGAAATATTTAAATGGTCTGT 950  
 317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
 951 GGTGCAAAAACATCCACACATGCCGTACTTTTGTGTATAACCATGATT 1000  
 334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
 1001 CTCAGCCCGGGGAGCATTGGATCTCTTGTTCACAAATGGTTAAACCA 1050  
 351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValph 367  
 1051 CTTGCATATGATGATGTTCTGCAAGGGAACAAGGTATCTCTCCGTATT 1100  
 367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384  
 1101 TTAATGGGATTAATCGGTATCCCAACCCATGCTTCCGGCTATGAAAT 1150  
 384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
 1151 CTAATAAGACCTCTCTCGAGGCACGTCAAACTTTTGCCTATGGTACG 1200  
 401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417  
 1201 CAGCATGATTAATTTGATCATCATGATATATATCGGTGGACAGAGAGG 1250  
 417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
 1251 AAATAGCTCCCATCAAAATTCAGGCCCTTGCACCATTTATGTCAGATGTC 1300  
 434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
 1301 CAGGTGTAACAAATGATGATGTTGGGAAAAAATAAGCGGGGACAGATT 1350  
 451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
 1351 TGGAGAGATATACCGGAAATAGGACAGGCACCGCTCACAATTAATGAGA 1400  
 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
 1401 CGGATGGGGTAATTTCTCTGTAAATGGAGGCTCGCTTTCGGTTGGGTGA 1450  
 484 ysGln 485  
 |||||

1451 AGCAA 1455

seq\_name: /SID2/jcgdata/geneseq/geneseqn/NA2000.DAT:AAA48480

seq\_documentation\_block:

ID AAA48480 standard; DNA; 1455 BP.

XX AC AAA48480;

XX DT 04-SEP-2000 (first entry)

XX DE Bacillus parent Termamyl-like alpha-amylase DNA sequence #1.

XX KW Bacillus; alpha-amylase; washing; textile desizing;

XX KW starch liquefaction; saccharification; mutein; mutant;

XX KW enzyme stability; hybrid; ss.

XX OS Bacillus sp.

XX FH Key Location/Qualifiers

XX CDS 1..1455

XX FT /\*tag= a

XX FT /product= "Termamyl-like alpha-amylase"

XX FT /partial

XX FN WO200029560-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-DK00628.

XX PR 16-NOV-1998; 98DK-0001495.

XX PA (NOVO ) NOVO-NORDISK AS.

XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX DR WPI; 2000-387777/33.

XX DR P-PSDB; AAY99602.

XX PT Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues .

XX PS Disclosure: Page 65-66; 80pp; English.

XX CC The present sequence encodes a parent Termamyl-like alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacillus genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the industrial processing of starch, i.e. starch liquefaction and saccharification. They may also be useful for washing, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created in order to increase enzyme stability.

XX SQ Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment\_scores:

Quality: 2613.00

Ratio: 5.421 Length: 485

Percent Similarity: 99.381

Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AAA48480 ..

Align seg 1/1 to: AAA48480 from: 1 to: 1455

```

1  HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1  CATCATANTGGAAACAAATGGTACTATGTCATAATATTCGAATGGTATTT 50
|||||
17  uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
|||||
51  GCCAAATGACGGGAATCATTTGGAAACAGTTGAGGGATGACGCAGCTAACT 100
|||||
34  euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||
101  TAAAGAGTAAAGGGATAACAGCTGTATGGATCCACCTGCATCGAAGGG 150
|||||
51  ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
|||||
151  ACTTCCCAAGATGATAGTTATGAGCCTATGATTTATATATGATCTGG 200
|||||
67  yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201  AGAGTTTAAACCAAGGGGACGCTTCGTACAAAATATGGAACACGCAACC 250
|||||
84  InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251  AGCTACAGGCTCGGTTGACCTCTTTAAAAAATAACGGCATTCAGGTATAT 300
|||||
101  GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301  GGTGATGTCGTATGATCATAAAGGTGGAGCAGATGGTACGGAAATGT 350
|||||
117  lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351  AAATCGGTTAGAAAGTGAATCGGAGCAACCGAAACAGGAAACCTCAGGAG 400
|||||
134  LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401  AGTATCAATAGAAAGCTGGACAAAGTTTGAATTTCTCTGGAAGAGGAAAT 450
|||||
151  ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451  AACCATTCAGCTTTAAGTGGCGCTGATCATATTTGATGGGACAGATTG 500
|||||
167  pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501  GGATCAGTCACGCCAGCTTCAAAACAAATATATAAATTCAGGGGAACAG 550
|||||
184  lYlYsAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551  GCAAGGCTGGGACTGGGAAGTCGATACAGAGAAATGGCAACTATGACTAT 600
|||||
201  LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601  CTTATGTATGCAGACCTGGATATGGATACCCAGAGTAATACATGAACT 650
|||||
217  uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651  TAGAAATCGGGAGTGTGGTATACGAATACACTGAACTTGATGGATTGA 700
|||||
234  rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701  GAATAGATGCAGTGAACACATATAAATATAGCTTTACGAGAGATTGGCTT 750
|||||
251  ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751  ACACATGTCGGTAAACACCAGCAGGTAACCAATGTTTGCAGTGCTGAGTT 800
|||||
267  eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
|||||
801  TTGGAATAAATGACCTTGGTGCAATTTGAAACACTATTTGAATAAAACAAGTT 850
|||||
284  rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851  GGAATCACTCGGTGTTGATGTTCTCTCCACTATAATTTGTACAATGCA 900
|||||

```

```
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGTGTATTATGATATGAGAAATATTTAAATGTTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTGCAAAACATCCACACATGCGGTACTTTTGTGATAACCATGATT 1000
|||||
334 erGlnProGlyGluAlaLeuGlnSerPheValGlnSerTyrPheLysPro 350
|||||
1001 CTCAGCCGGGGAAGCAATGGAATCTTTGTTCAACAATGGTTTAAACCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGlnGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCATATGCAATGGTCTCTGACAAGGAACAAGTTATCTCTCCGTATT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
|||||
1101 TTAATGGGATTAATGCTATGCTATCCCAACCCATGGTTCCGGCTATGAAT 1150
|||||
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAATAATAGACCTCTCTCTGAGCAGCTCAACTTTTGCTATGTGACG 1200
|||||
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrThrArgGluG 417
|||||
1201 CAGCATGATTACTTTGATCATCATGATATTTATCGTTGGACAAGAGGG 1250
|||||
417 YAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AATAGCTCCATCCCAATTCAGCCCTTGCCACCATTTATGTCAGATGTC 1300
|||||
434 roGlyGlyAsnLysTyrMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGTAACAAATGATGATGTGGGAAATAAAGCGGACAAAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATTACCGGAATAGGACAGGACCGTCACAAATTAATGCGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
|||||
1401 CGGATGGGGTAATTTCTCTTAATGAGGGTCGCTTCGGTTGGGTGA 1450
|||||
484 ySgln 485
|||||
1451 AGCAA 1455
```

seq\_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48485

```
seq_documentation_block:
ID AAA48485 standard; DNA; 1455 BP.
XX
AC AAA48485;
XX
DE 04-SEP-2000 (first entry)
XX
KW Bacillus Termamyl-like alpha-amylase DNA sequence #3.
KW starch liquefaction; washing; textile desizing;
KW enzyme stability; hybrid; ss.
XX
OS Bacillus sp.
XX
PH Key Location/Qualifiers
FT CDS 1..1455
FT /*tag= a
FT /product= "Termamyl-like alpha-amylase"
FT /partial
XX
PN WO200029560-A1.
```

XX  
PD  
XX  
PF  
XX  
PR  
XX  
PA  
XX  
PI  
XX  
XX  
XX  
PT  
PT  
XX  
PS  
XX  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
CC  
SQ

25-MAY-2000.  
16-NOV-1999; 99WO-DK00628.  
16-NOV-1998; 98DK-0001495.  
(NOVO ) NOVO-NORDISK AS.  
Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;  
WPI; 2000-387777/33.  
Variant of parent termamyl-like alpha amylase useful for washing,  
textile desizing and starch liquefaction, comprising alterations in one  
or more solvent exposed amino acid residues  
Disclosure; Page 69-70; 80pp; English.  
The present sequence encodes an alpha-amylase from which mutants  
with increased stability at acidic pH, low calcium concentration and high  
temperatures have been derived. The sequence was isolated from a Bacillus  
genomic DNA library. A variant may contain mutations in one or more  
solvent exposed amino acid residues to increase the overall  
hydrophobicity of the enzyme or the overall number of methyl groups in  
the side chains of exposed residues may be increased. The mutations can  
be incorporated by site-directed mutagenesis or by random mutagenesis. As  
a result of their increased stability, the variants are suitable for the  
industrial processing of starch, i.e. starch liquefaction and  
saccharification. They may also be useful for washing, dishwashing and  
textile desizing. Hybrid alpha-amylases comprising partial amino acid  
sequences derived from two or more alpha-amylases have also been created  
in order to increase enzyme stability.  
Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;

alignment\_scores:

Quality: 2613.00 Length: 485  
Ratio: 5.421 Gaps: 0  
Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AAA48485

Align seg 1/1 to: AAA48485 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
|||||  
1 CATCATATGGAACAATGGTACTATGATGCAATATTTCAATGGTATTT 50  
|||||  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34  
|||||  
51 GCCAAATGACGGGAATCATTTGGAAACAGTTGAGGGATGACGACGTAAC 100  
|||||  
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50  
|||||  
101 TAAAGAGTAAAGGGATAACAGCTGTATGGATCCACCTGCATGGAAGGG 150  
|||||  
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67  
|||||  
151 ACTTCCCAAGATGATGATGTTATGGAGCTATGATTTATATGATCTGG 200  
|||||  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
|||||  
201 AGAGTTTAAACCAAGAGGGACGGTTCGTACAAAATATGGAACACGCAACC 250  
|||||  
84 lnteuGlnGlyAlaValThrSerLeuLysAsnAsnGlylleGlnValTyr 100  
|||||  
251 AGCTACAGGCTCGGTGACCTCTTTAAAAAATAACGGCATTGAGGTATAT 300  
|||||  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||

301 GGTGATGTCGTCATGAATCAATAAAGGTGGAGCAGATGTCACGGAATGT 350  
117 lasAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
351 AAATGCGGTAGAGTGAATCGGAGCAACCGAACCAGGAACCTCAGGAG 400  
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
401 AGTATGCAATAGACGCTGGACAAAGTTTGATTTTCCTGGAAGAGAAAT 450  
151 ThrHisSerAsnPheLysTrpArgTrpThrHisPheAspGlyThrAspTr 167  
451 AACCATTCCAGCTTAACTGGCGTGGTATCATTTTGATGGACAGATTG 500  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
501 GGATCAGTCACGCCAGCTTCAAAACAAATATATAAATTCAGGGGAACAG 550  
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlnAsnTyrAspTyr 200  
551 GCAAGGCTGGGACTGGGAAGTCGATACAGAGAAATGCAACTATGACTAT 600  
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
601 CTTATGTATGACAGCTGGATATGATGATCACCAGAAATTAATACATGAACT 650  
217 uArgAsnTrpGlyValTyrTrpThrAsnThrLeuAsnLeuAspGlyPheA 234  
651 TAGAACTGGGAGTGTGTATACGAATACACTGAACCTTGATGGATTTA 700  
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
701 GAATAGATGCAGTGAACATATATAAATATAGCTTTACGAGAGATTGGCTT 750  
251 ThrHisValArgAsnThrGlyLysProMetPheAlaValAlaGluPh 267  
751 ACACATGTCGCTAACACACAGGTAAACCAATGTTTGCAGTGGCTGAGTT 800  
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
801 TTGGAAAAATGACCTTGGTGCATTTGAAACTATTTGATTAACAAGTT 850  
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
851 GGAATCACTCGGTGTGTATGTTCTCTCCACTATAATTTGTACAATGCA 900  
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
901 TCTAATAGCGGTGTTATATGATATGAGAAATATTTTAAATGGTCTGT 950  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
951 GGTGCAAAACATCCACACATGCGCTTACITTTTCTTGATAACCATGATT 1000  
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
1001 CTCAGCCGGGGAAGCATTTGGAATCCTTGTTCACAACAAATGGTTAAACCA 1050  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValph 367  
1051 CTTGCATATGCAATGGTCTGTGACAAAGGAACAAGGTTATCTCTCGGTATT 1100  
367 eTyrGlyAspTyrGlyIleProThrHisGlyValProSerMetLysS 384  
1101 TTATGGGATTAATACGATATCCCAACCCATGGTGTTCGGGTATGAAT 1150  
384 erLysIleAspProLeuLeuGlnAlaIleArgGlnThrTyrAlaTyrGlyThr 400  
1151 CTAAATAGACCTCTCTGACGACGACGCAAACTTTTGCCTATGCTAGC 1200  
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrTrpArgGluG 417  
1201 CAGCATGATTAATTTGATCATCATGATATATATCGGTGGCAAGAGAGG 1250

417 yAspSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
1251 AAATAGCTCCCATCCAAATTCAGGCTTCGCCACCATTTATGTCAGATGCTC 1300  
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
1301 CAGGTGGTAAACAAATGGATGTATGTGGGAAAAATAAAGCGGACAGTT 1350  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
1351 TGGAGAGATATTACCGAAATAGGACAGCGCCGTCACAAATTAATGCGAGA 1400  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
1401 CGGATGGGGTAATTTCTCTGTTAATGAGGGTCCGTTTCGGTTGGGTGA 1450  
484 ysgln 485  
1451 AGCAA 1455

seq\_name: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:AAx57592

seq\_documentation\_block:

ID AAX57592 standard; DNA; 1455 BP.

XX AAX57592;

XX 16-JUL-1999 (first entry)

XX Wild type Termamyl(RTM)-like alpha-amylase coding sequence #1.

XX Variant: Termamyl; alpha-amylase; mutation: Bacillus; detergent;

XX dishwashing; laundry; textile; desizing; starch liquefaction;

XX sweetener; ethanol; ss.

XX Bacillus sp.

XX WO9919467-A1.

XX 22-APR-1999.

XX 13-OCT-1998; 98WO-DK00444.

XX 13-OCT-1997; 97DK-0001172.

XX (NOVO ) NOVO-NORDISK AS.

XX Bisgard-Frantzen H, Borchert TV, Svendsen A;

XX WPI; 1999-277632/23.

XX Variant alpha-amylases - useful as detergents or for textile

XX desizing or starch liquefaction

XX Disclosure; Page 76-77; 93pp; English.

XX This sequence represents the coding sequence for a parent sequence  
used to generate new variants of a Termamyl-like alpha-amylase with  
alpha-amylase activity. The variants comprise mutations in 2-6  
regions/positions relative to an alpha-amylase from either of two  
Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis,  
B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants  
are detergent additives for use in detergents for dishwashing, manual  
or automatic laundry. The variants can also be used for textile desizing  
or starch liquefaction (e.g. for production of sweeteners or ethanol).

XX Sequence 1455 BP; 463 A; 246 C; 361 G; 385 T; 0 other;

alignment\_scores:

Quality: 2601.00

Ratio: 5.396

Length: 485

Gaps: 0

Percent Similarity: 99.381		Percent Identity: 94.433	
alignment_block:			
US-09-590-375-2 x AAX57592			
Align seg 1/1 to: AAX57592 from: 1 to: 1455			
1	HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe	17	
1	CATCATATGCAACAAATGGTACTATGATGCAATATTCGAATGGTATT	50	
17	uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL	34	
51	GCCAAATGACGGGAATCATTTGAACAGGTGTAGGGATGACGAGTAACT	100	
34	eulysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly	50	
101	TAAAGAGTAAAGGATACAGCTGTATGGATCCCACTGCATGGAAGGG	150	
51	ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl	67	
151	ACTTCCAGAAATCATGTAGGTTATGGAGCCTATGATTTATATGATCTGG	200	
67	yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG	84	
201	AGAGTTTAAACCAAGGAGCGGTTTCGTACAAATATGGAACACGCAACC	250	
84	lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr	100	
251	AGCTACAGGCTGGGTGACCTCTTTAAATAAATACGGCATTCAGGTATAT	300	
101	GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa	117	
301	GGTGATGCTGTCATGAATCAATAAGGTGGAGCAGATGGTACGGAATTGT	350	
117	lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG	134	
351	AAATGCGGTAGAGTGAATCGGAGCAACCCAGGAACCCCTCAGGAG	400	
134	luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn	150	
401	AGTATGCAATAGAACGCTGGCAAAAGTTTATTTCTCGGAAGAGGAAT	450	
151	ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr	167	
451	AACCATCCAGCTTTAAGTCGCGTGTATCATTTTTCATGGCAGAGATTG	500	
167	pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG	184	
501	GGATCAGTCACGATCAGTCAAAAAACAAATATATAAATTCAGGGGAAC	550	
184	lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr	200	
551	GCAAGGCTGGGACTGGGAATGCATACAGAGATGGCAACTATGACTAT	600	
201	LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe	217	
601	CTTATGTATGCAGACGTGGATATGGATCACCAGAAAGTAATACATGACT	650	
217	uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA	234	
651	TAGAAACTGGGGAGTGTGGTATACGAATACACTGAACCTTGATGGATT	700	
234	rgileAspAlaValLysHisIleLysTrpSerTyrThrArgAspTrpLeu	250	
701	GAATAGATGCAGTGAACATATAAATATAGCTTTACGAGAGATTGGCTT	750	
251	ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh	267	
751	ACACATGTGCGTAAACACACAGGTAAACAAATGTTTGCAGTGGCTGAGT	800	
267	enrPlysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT	284	

801	TTTGGAAAAATGACCTTGGTGCATTTCAAACACTATTTTGAATAAAACAAGTT	850
284	rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla	300
851	GGAAATCACCTCGGTGTTTGATGTTTCTCTCCACTATATAATTTGTACAAATGCA	900
301	SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa	317
901	TCTTAATAGCGGTGGTTATTATGATATGAGAAATATTTTAAATGGTTCTGT	950
317	lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS	334
951	GGTGCAAAAAACATCCCAACACATGCCGTACTTTTGTGATAACCATGATT	1000
334	erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro	350
1001	CTCAGCCCGGGGAAGCATTTGGAATCTTTGTTCAACAATGGTTTAAACCA	1050
351	LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh	367
1051	CTTGCAATATGCATTGGTTCTGACAGGGAACAGGTTATCTCTCCGTATT	1100
367	eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS	384
1101	TTATGGGGATTACTACGGTATCCCAACCCATGGTTCGCGCTATGAAT	1150
384	erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr	400
1151	CTAAATAGACCCTCTCTGCAGGCACGTCAAACCTTTTGCTATGTGTACG	1200
401	GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl	417
1201	CAGCATGATTACTTTGATCATCATGATATTATCGTTGGACAAGAGAGG	1250
417	yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP	434
1251	AAATAGCTCCCATCAAAATTCAGSCCTTGCACCATTTATGTCAGATGGTC	1300
434	roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal	450
1301	CAGGTGGTAACAAATGGATGTATGTGGGAAAAATAAAGCGGCAACAGTT	1350
451	TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs	467
1351	TGGAGAGATATACCGGAATAGGACAGGCACCGTCACAATTAATGCAGA	1400
467	pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL	484
1401	CGGATGGGGTAATTTCTCTGTTAATGGAGGGTCGCTTTCGGTTTGGGTGA	1450
484	ysGln	485
1451	AGCAA	1455
seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT.AAX59633		
seq_documentation_block:		
ID	AAX59633 standard; DNA; 1455 BP.	
XX	AAX59633;	
AC	AAX59633;	
XX	22-JUL-1999 (first entry)	
DT	22-JUL-1999 (first entry)	
XX	DNA encoding a termamyl-like alpha-amylase protein.	
DE	Termamyl-like; alpha-amylase; variant; washing; dishwashing;	
XX	production; sweetener; ethanol; starch; textile desizing;	
KW	starch liquefaction; saccharification process; ss.	
KW	Bacillus sp.	
OS	WO9923211-A1.	
XX		
PN		
XX		

seq\_name: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT: AAX59633  
seq\_documentation\_block:  
ID AAX59633 standard; DNA; 1455 BP.  
XX  
AC AAX59633;  
XX  
DT 22-JUL-1999 (first entry)  
XX  
DE DNA encoding a termamyl-like alpha-amylase protein.  
XX  
KW Termamyl-like; alpha-amylase; variant; washing; dishwashing;  
KW production; sweetener; ethanol; starch; textile desizing;  
KW starch liquefaction; saccharification process; ss.  
XX  
OS Bacillus sp.  
XX  
PN W0923211-A1.  
XX



PD 14-MAY-1999.  
 XX  
 PF 30-OCT-1998; 98WO-DK00471.  
 XX  
 PR 14-JUL-1998; 98DK-0000936.  
 PR 30-OCT-1997; 97DK-0001240.  
 XX  
 XX (NOVO ) NOVO-NORDISK AS.  
 PA  
 XX  
 PI Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;  
 PI Nissen TL, Svendsen A;  
 XX  
 DR WPI; 1999-326987/27.  
 XX  
 PT New Termamyl-like alpha-amylase variants  
 XX  
 PS Disclosure; Page 92-93; 115pp; English.  
 XX  
 CC The specification describes termamyl-like alpha-amylase variants that  
 CC have altered amino acid sequences to improve properties. The variants  
 CC are produced by creating one or more of the following mutations in  
 CC amino acid sequence of the parent termamyl-like alpha-amylase: R141,  
 CC K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183,  
 CC G184, K185, A186, W189, S193, M195, H107, K108, G109, D166, W167, D168,  
 CC Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273,  
 CC A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462,  
 CC T463. The variants can be used for washing and/or dishwashing. They can  
 CC also be used in the production of sweeteners and ethanol from starch,  
 CC and/or for textile desizing, and in starch liquefaction and/or  
 CC saccharification processes. The present sequence encodes an amylase  
 CC that can function as the parent sequence in the production of the  
 CC variants of the invention.  
 XX  
 SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment\_scores:  
 Quality: 2440.00 Length: 485  
 Ratio: 5.148 Gaps: 0  
 Percent Similarity: 97.732 Percent Identity: 86.598

alignment\_block:  
 US-09-590-375-2 x AAX59633 ..  
 Align seg 1/1 to: AAX59633 from: 1 to: 1455

```

1 H1SH1SAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCATATGGGCAAAATGGGACGATGATGCAATACTTTGAATGGCACTT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAsnL 34
|||||
51 GCCTAATGATGGGAATCACTCGAATAGATTAAGAGATGATCTAGTAATC 100
|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
|||||
101 TAAGAAATAGAGTATAACCCCTATTGGATTCCGCTCGCTGGAAGGG 150
|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuGly 67
151 ACTTCGCAAAATGATGTGGGTATGGAGCCCTATGATCTTTATGATTAGG 200
|||||
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 GGAATTAATCAAAAGGGGACGGTTCGTACTAAGTATGGGACAGCTAGTC 250
|||||
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AATTGGAGCTCTGCCATCCATCTTTAAAGAATAATGGCGTTCAAGTTAT 300
|||||
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGGGATGTAGTGAACCATAAAGGAGGAGCTGATGCTACAGAAACGT 350

```

```

117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351 TCTTGTCTGCGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGG 400
|||||
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 ACTACACAATTTAGGCTTGGACTAAGTTTGATTTTCCAGGGAGGGTAAT 450
|||||
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTCCGATGGTGTAGATTG 500
|||||
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAATCAGCACAATTCNAATCGTATCTACAAATTCGAGGTGATG 550
|||||
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GTAAGGCATGGGATGGGAAGTAGATTCCGAAATGGAATATATGATTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 TTAATGATATGCAGATGATGATGATGATCCGAGGTAGTAAATGAGCT 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAGATGGGCAAAATGGTATACAAATACATTAATCTTGATGATTTA 700
|||||
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GCATCGATCGGTGAAGCATATTAATATAGCTTTACACGTGATTGGTTG 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACCCATGTAAGAAACGCAACGGGAAAGAAATGTTGCTGTGCTGAATT 800
|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
|||||
801 TTGCAAAATGATTTAGTGCCTGGAGAACTATTTAAATAAACAACACT 850
|||||
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCATCTGCTTTGATGTCCTCCCTTCATTTAATCTTTATAACGCG 900
|||||
301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCAATATAGTGGAGGCAACTATGACATGGCAAAACTTCTTAATGGAACGGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 TGTTCAAAAGCATCCAATGCGATCGCTAACTTTTGGATAATCACCATT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAACCTGGGGAATCATTTAGATCATTTGTACAGAAGTGGTTTAAAGCCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCTTATGCGCTTATTTTAAAGAGAGAACAAAGGCTATCCCTCTGCTCT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 CTATGGTGACTACTATGGAATTCACACATAGTGTCCACGAATGAAG 1150
|||||
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CCAAGATTGATCCAATCTTAGAGCGGCTCAAAATTTTGTATATGGAACA 1200
|||||
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl 417
|||||
1201 CAACATGATTATTTTGACCATCAATAATAATCGGATGGACACGTAAGG 1250

```





117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
351 TCTTGCCTGTCGAGGTGAATTCACCAATTAACCGGAATCAAGAAATATCTGGG 400  
134 LuTyThrIleGluAlaThrLysPheAspPheProGlyArgClyAsn 150  
401 ACTACACAATTCGAGCTTGGAGTAAGTTTGATTTTCCAGGAGGGGTAAAT 450  
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
451 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTTCGATGCTGTAGATTG 500  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
501 GGATCAATCAGACAAATCCAAAATCGTATCATCAAAATCCGAGGTGATG 550  
184 LylsAlaIleAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
551 GTAAGCATGGGATTTGGCAAGTAGATTCGGAATAATGGAATTTATGATTAT 600  
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
601 TTTAATGTATGCAGATGTAGATGGATCATCCGAGAGGTAGTAAATGAGCT 650  
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
651 PAGAAGATGGGAGAAATCGTATACAAATACATTAATCTTGATGGATTATA 700  
234 rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
701 GGATCGATCGCGTGAAGCATATTAATATAGCTTACACGTGATGGTGTG 750  
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
751 ACCCATGTAAAGAACCCCAACGGGAAAGAAATGTTTCTGTGTCTGAATT 800  
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
801 TTGGAAAAATGATTTAGCTGCCTTGGAGACAATATTTAAATAAAACAACT 850  
284 tPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
851 GGAATCATCTGCTTTGATGTCCTTCATTAATATATATCTTTATAACGGG 900  
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
901 TCAAAATAGTGAGGCAACTATACATGSCAAAACCTTCTTAATGGAACGGT 950  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334  
951 TGCTTCAAAGCATCCAAATGCATGCGGTAACTTTTGTGGTAAATCACCATT 1000  
334 eRGlnProGlyGluAlaLeuGlnSerPheValGlnSerTrpPheLysPro 350  
1001 CTCACCTGGGGAATCATTAATCATTTGTACAGAATGGTTTAAGCCA 1050  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
1051 CTTCGTTATGGCTTATTTTAAAGAAGACAAGCGTATCCCTCTGTCTT 1100  
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384  
1101 CTATGGTGACTACTATGGAATTTCCACACATAGTGTCCACGCAATGAAG 1150  
384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
1151 CCAAGATGATCCAATCTTAGAGCGCGCTCAAAATTTTGCATATGGAACA 1200  
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417  
1201 CAACATGATTTTGGACCATCAATATTAATCGATGGACACGTGAAGG 1250  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434

```

|||||.....
1251 AAATACCGCATCCCAATTAGGACTTCGGACTTATCATGTGGATGGGC 1300
      |||||.....
434   roGlyGlyAsnLysTrpMetTyrrValGlyLysHisLysAlaGlyGlnVal 450
      |||||.....
1301 CAGGGGGCAGAGAAATGGATGTACGTAGGCCAAAATAAAGCAGGTCAAGTT 1350
      |||||.....
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
      |||||.....
1351 TGGCATGACATAACTGGAAATAAACCCAGGAACAGTTACGATCAATGCAGA 1400
      |||||.....
467 pGlyTpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
      |||||.....
1401 TGGATGGGGTAATTTTCAGTAAATGGAGAGACTGTTTCCATTTGGTGCA 1450
      |||||.....
484 ysGln 485
      ||:::
1451 AACGA 1455

seq_name: /SIDS2/gcgdata/geneseq/geneseqp/NA1999.DAT:AXX57598
seq_documentation_block:
XX ID AAX57598 standard; DNA; 1455 BP.
XX AC
XX AAX57598;
XX DT
XX 16-JUL-1999 (first entry)
XX DE Wild type Termamyl(RTM)-like alpha-amylase coding sequence #
XX KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction;
KW sweetener; ethanol; ss.
XX OS Bacillus sp.
XX PN W099919467-A1.
XX PD 22-APR-1999.
XX PF 13-OCT-1998; 98WO-DK00444.
XX PR 13-OCT-1997; 97DK-0001172.
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Bisgard-Frantzen H, Borchert TV, Svendsen A;
XX DR WPT; 1999-277632/23.
XX PT Variant alpha-amylases - useful as detergents or for textil
XX desizing or starch liquefaction
XX PS Disclosure; Page 84-85; 93pp; English.
XX CC This sequence represents the coding sequence for a parent se
XX used to generate new variants of a Termamyl-like alpha-amyla
XX alpha-amylase activity. The variants comprise mutations in
XX regions/positions relative to an alpha-amylase from either o
XX Bacillus species in W09526397, B. stearothermophilus, B. lic
XX B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylas
XX are detergent additives for use in detergents for dishwashin
XX or automatic laundry. The variants can also be used for text
XX or starch liquefaction (e.g. for production of sweeteners or
XX Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other:
SQ
```

alignment_scores:		
Quality:	2440.00	Length: 485
Ratio:	5.148	Gaps: 0
Percent Similarity:	97.732	Percent Identity: 86.598

alignment\_block:

US-09-590-375-2 x AAX57598

Align seg 1/1 to: AAX57598 from: 1 to: 1455

```

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
1 CATCATATGGGACAAATGGGACGATGATGCAATACCTTTGAATGGCACTT 50
17 uProAsnAspGlyAsnHisTrpAsnArgLeuAspAspAlaAlaAsnL 34
|||||
51 GCCTAATGATGGGAATCAGTGAATAGATTAAGAGATGATGCTAGTAATC 100
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
|||||
101 TAAGAATAGAGGTATACCCGCTATTTGGATTCGCCCTGCCGCGAAAGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTrpHisLe 67
151 ACTTCGCAAAATGATGTGGGTATGGAGCTATGATCTTTATGATTTAGG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 GGAATTTAATCAAAAGGGAGCGTTCGTACTAAGTATGGGACAGCTAGTC 250
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AATTGGAGTCTGCCATCCATGCTTTAAGAATAATGGCGTTCAAGTTAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
301 GGGGATGATGATGAACCAATAAAGGAGGAGCTGATGCTACAGAAAACGT 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnLysSerGlyG 134
|||||
351 TCTTGTCTCGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGG 400
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 ACTACAAATGAGCGTTGGACTAAGTTTGTATTTCCAGGAGGGGTAAT 450
151 ThrHisSerAsnPheLysTyrArgTyrTrpHisPheAspGlyThrAspTr 167
451 ACATACTCAGACTTTAAATGCGTGTGGTATCATTTCCGATGCTGTAGATTG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAATCAGCAATTCCAAAATCGTATCTACAAATTCGAGGTGATG 550
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GTAAGGCATGGGATGGGAAGTACATTCGGAATAATGGAATATGATAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 TTAATGATGACAGATGATAGATATGATCATCCGGAGGTAGTAAATGAGCT 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAGATGGGGAGATGGGTATACAAATACATTAATCTTCATGGATT 700
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GGATCGATGGGTCAAGCATATTAATATAGCTTTACACGTGATGGTTG 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
751 ACCCATGTAGAAAACGCAACCGGAAAAAGAAATGTTGCTGTGCTGAATT 800
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGAAAAAATGATTAGTGCTTGGGAGAACTATTTAAATAAAACAAACT 850

```

```

284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCATCTGCTTTGATGTCCTCCCTTCATTATATCTTTATAACGGC 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
901 TCAATAGTAGGAGCAACTATGACATGCAAAACTCTCTTAATGGAAGGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
951 TGTTCAAAAGCATCCAAATGCATCCGTAACCTTTGTGGATAATCACCATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
1001 CTCACCTGGGAATCATAGAACATTTGTACAGAATGGTTTAAGCCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
1051 CTTGCTTATGCGCTTATTTTAAACAAGAGAACACAGGCTATCCCTCTGCTT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
1101 CTATGGTGACTACTATGGAATTCACACATAGTGTCCACGAATGAAG 1150
384 erLysIleAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
1151 CCAAGATTGATCCAATCTAGAGCGCGTCAAAATTTTGCATATGGAACA 1200
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417
1201 CAACATGATTATTTTGACCATCATATAATATCGGATGGACACGTGAAG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1251 AAATACCACGCATCCCAATTCAGGACTTCGACATATCATGTGCGATGGGC 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1301 CAGGGGAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1351 TGGCATGACATAACTGGAAATAAACACAGGAACAGTTACGATCAATGCA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
1401 TGGATGGCTAAATTTTTCAGTAAATGGAGGATCTGTTTCCATTGGGTGA 1450
484 ysGln 485
|||||
1451 AACGA 1455

seq_name: /SDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48481
seq_documentation_block:
ID AAA48481 standard; DNA; 1455 BP.
XX
AC AAA48481;
XX
DT 04-SEP-2000 (first entry)
XX
DE Bacillus parent Termamyl-like alpha-amylase DNA sequence #2.
XX
KW Bacillus; alpha-amylase; washing; textile desizing;
KW starch liquefaction; saccharification; mutein; mutant;
KW enzyme stability; hybrid; ss.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..1455
FT /tag= a
FT /product= "Termamyl-like alpha-amylase"

```

FT XX /partial

PN W0200029560-A1.

XX 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-DK00628.

XX PR 16-NOV-1998; 98DK-0001495.

XX PA (NOVO ) NOVO-NORDISK AS.

XX PI Svendsen A, Kjaerulff S, Bisgard-Prantzen H, Andersen C;

XX DR WPI: 2000-387777/33.

XX DR P-PSDB: AAY99603.

XX Variant of parent termamyl-like alpha amylase useful for washing,  
PT textile desizing and starch liquefaction, comprising alterations in one  
PT or more solvent exposed amino acid residues -

XX PS Disclosure; Page 66-67; 80pp; English.

XX CC The present sequence encodes a parent Termamyl-like alpha-amylase  
CC from which mutants with increased stability at acidic pH, low calcium  
CC concentration and high temperatures have been derived. The sequence was  
CC isolated from a Bacillus genomic DNA library. A variant may contain  
CC mutations in one or more solvent exposed amino acid residues to increase  
CC the overall hydrophobicity of the enzyme or the overall number of  
CC methyl groups in the side chains of exposed residues may be increased.  
CC The mutations can be incorporated by site-directed mutagenesis or by  
CC random mutagenesis. As a result of their increased stability, the  
CC variants are suitable for the industrial processing of starch, i.e.  
CC starch liquefaction and saccharification. They may also be useful for  
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases  
CC comprising partial amino acid sequences derived from two or more  
CC alpha-amylases have also been created in order to increase enzyme  
CC stability.

XX SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment\_scores:

Quality: 2440.00 Length: 485  
Ratio: 5.148 Gaps: 0  
Percent Similarity: 97.732 Percent Identity: 86.598

alignment\_block:

US-09-590-375-2 x AAA48481 ..

Align seg 1/1 to: AAA48481 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17

|||||

1 CATCATATGGGCAAAATGGGACGATGATGCAATCTTTGAATGGCACTT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAsnL 34

|||||

51 GCCTATGATGGGAATCACTGGGAATAGATTAAGACATGATGCTAGTAATC 100

34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50

|||||

101 TAGAANAATAGAGTATAACCGTATTTGGATTCGCCCTGCCCTGGAAAGG 150

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67

|||||

151 ACTTCGCAAAATGATGGGATGGGATGGAGCCTATGATCTTTATGATTAGG 200

67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84

|||||

201 GGAATTTAATCAAAAGGGACGGTTTCGTACTAAGTATGGACACACGTAGTC 250

84 lnLeuGlnGlyAlaValThrSerLeuLysAsnGlyIleGlnValTyr 100

251 AATGGAGCTGCCCATCCATGCTTTAAAGAATAATGGCGTTCAGTTTAT 300  
|||||

101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||

301 GGGGATGATGATGAACCATAAAGGAGGAGCTGATGCTACAGAAACGT 350  
|||||

117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
|||||

351 TCTTGCTGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGG 400  
|||||

134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
|||||

401 ACTACACAATTCAGGCTTGGACTAAGTTTGATTTTCCAGGGAGGGTAAT 450  
|||||

151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
|||||

451 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTCCGATGGTGTAGATTG 500  
|||||

167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
|||||

501 GGATCAATCAGCACAAATCCAAATCGTATCTACAAATTCGAGGTGATG 550  
|||||

184 lYlAsAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
|||||

551 GTAAGGCATGGGATGGGAAGTAGATTTCGAAATGGAAATTTATGATTAT 600  
|||||

201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
|||||

601 TTAATGATGATGAGATGATGATGATGATCGGAGGTAGTAATAGAGCT 650  
|||||

217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
|||||

651 TAGAAGATGGGAGAGATGATGATACAAATACATTAATCTTGATGATTTA 700  
|||||

234 tqLleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
|||||

701 GGATCGATCGGTGAAGCATATTAATATAGCTTTACACGATGATGGTTG 750  
|||||

251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
|||||

751 ACCCATGTAAGAAACGCAACGGAAGAAATGTTGCTGTTGCTGAATT 800  
|||||

267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
|||||

801 TTGGAAATATGATTTAGGTGCGCTGGAGAACATTTAAATAAAACAACT 850  
|||||

284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
|||||

851 GGAATCATCTGCTTGTGATGTCCTTCATTAATAATCTTTATAACGCG 900  
|||||

301 SerAsnSerGlyTyrTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
|||||

901 TCAAAATAGTGGAGCAACTATGACATGCGCAAACTCTTTAATGGAACGCT 950  
|||||

317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
|||||

951 TCTTCAAAAGCATCAATGATGCGTAACCTTTTGGGATAATCAGATT 1000  
|||||

334 exGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
|||||

1001 CTCACCTGGGAATCATTTAGAATCATTTGTACAGAATGGTTTAAGCCA 1050  
|||||

351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
|||||

1051 CTGTGTTATGCGCTTATTTTAAAGAGAACCAAGGCTATCCCTCTGCTT 1100  
|||||

367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384  
|||||

1101 CTAATGCTGACTACTATGGAATTCACACATAGTGTCCAGCAATGAAG 1150  
|||||

384 exLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
:::|||||

1151 CCAAGATTGATCCAAATCTTAGAGCGCGTCAAAATTTTGCATATGGAACA 1200  
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG1 417  
1201 CAACATGATATTTTGGACCATCATATATATCGGATGGACACGTGAAGG 1250  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
1251 AAATACCACGCATCCCAATTCAGGACTTGGACTATCATGTGCGGATGGC 1300  
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
1301 CAGGGGAGAGAGATGATGTACGTAGGCAAAATAAGCAGGTCAAGTT 1350  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
1351 TGGCATGACATACCTGGAATAACACAGGAACAGTTACGATCAATGCAGA 1400  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
1401 TGGATGGCTAAATTTTCAGTAAATGAGGATCTGTTTCCATTGGGTGA 1450  
484 ySGln 485  
1451 AACGA 1455

seq\_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48486

seq\_documentation\_block:

ID AAA48486 standard; DNA; 1455 BP.

XX AC AAA48486;

XX DT 04-SEP-2000 (first entry)

XX DE Bacillus Termamyl-like alpha-amylase DNA sequence #4.

XX KW Bacillus; alpha-amylase; washing; textile desizing;  
KW starch liquefaction; saccharification; mutein; mutant;  
KW enzyme stability; hybrid; ss.  
XX OS Bacillus sp.

XX FH Key

FT CDS Location/Qualifiers

FT 1..1455

FT /\*tag= a

FT /product= "Termamyl-like alpha-amylase"

FT /partial

XX PN WO200029560-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-DK00628.

XX PR 16-NOV-1998; 98DK-0001495.

XX PA (NOVO ) NOVO-NORDISK AS.

XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX DR WPI; 2000-387777/3.

XX DR P-PSDB; AAY99609.

XX PT Variant of parent termamyl-like alpha amylase useful for washing,  
PT textile desizing and starch liquefaction, comprising alterations in one  
PT or more solvent exposed amino acid residues -  
XX PS Disclosure; Page 70-71; 80pp; English.

XX CC The present sequence encodes a parent alpha-amylase from which mutants  
CC with increased stability at acidic pH, low calcium concentration and high  
CC temperatures have been derived. The sequence was isolated from a Bacillus

CC genomic DNA library. A variant may contain mutations in one or more  
CC solvent exposed amino acid residues to increase the overall  
CC hydrophobicity of the enzyme or the overall number of methyl groups in  
CC the side chains of exposed residues may be increased. The mutations can  
CC be incorporated by site-directed mutagenesis or by random mutagenesis. As  
CC a result of their increased stability, the variants are suitable for the  
CC industrial processing of starch, i.e. starch liquefaction and  
CC saccharification. They may also be useful for washing, dishwashing and  
CC textile desizing. Hybrid alpha-amylases comprising partial amino acid  
CC sequences derived from two or more alpha-amylases have also been created  
CC in order to increase enzyme stability.  
XX SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment\_scores:

Quality: 2440.00 Length: 485

Ratio: 5.148 Gaps: 0

Percent Similarity: 97.732 Percent Identity: 86.598

alignment\_block:

US-09-590-375-2 x AAA48486

Align seg 1/1 to: AAA48486 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
1 CATCATATGGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTT 50  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34  
51 GCCTAATGATGGGAATCACTGGAATAGATTAAAGAGATGATCTAGTAATC 100  
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50  
101 TAGAAATAGAGGTATAACCGCTATTTTGGATTCCGCTCGCTGGAAGGG 150  
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG1 67  
151 ACTTCGCAAAATGATGTGGGTATGGAGCTATGATCTTTATGATTAGG 200  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
201 GGAATTTAATCAAAAGGGGACGGTTCTGTAAGTATGGGACACGTAGTC 250  
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
251 AATTGGAGTCTGCCATCCATGCTTTAAAGAAATAATGGCGTTCAAGTTAT 300  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
301 GGGGATGCTAGTGTAGTAACCATAAAGGAGGAGCTGATGCTACAGAAACGT 350  
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
351 TCTTGCCTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGG 400  
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
401 ACTACAAATGGAGCTTGGACTAAGTTTATTTCCAGGGAGGGGTAAT 450  
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
451 ACATACCTACAGACTTTAAATGGCGTTGCTATCATTTCCGATGGTAGATTG 500  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
501 GGATCAATCAGCACATTCGAAATCGTATCTACAAATTCGAGGTGATG 550  
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
551 GTAAGGCATGGGATTGGGAAGTAGATTTCGGAAATGGAATATGATGATTAT 600

201	LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLeu	217
601	TTAATGTATGCAGATGTAGATATGGATCATCCGGAGGTAGTAATAAGACCT	650
217	uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA	234
651	TAGAAGATGGGGAGAATGGTATACAATACATTAATCTTGATGATTATA	700
234	rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu	250
701	GGATCGATGCCGTGAAGCATATTAAATATAGCTTTACACGTCATTGGTGTG	750
251	ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh	267
751	ACC CATGTAGA AACGCAACGGG AAGAAAAT GTTTGCTGTGCTGTAAT	800
267	eTrpLysAsnAspLeuAlaLalIleGluAsnTyrLeuAsnLysThrSerT	284
801	TTGGAAAAATGATTTTAGTGGCCTGGAGAACATATTAAATAAAACAACT	850
284	rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla	300
851	GGAATCATTCGTCTTGTGATGTCGCCCTTCATTATATATCTTTATAACGCG	900
301	SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa	317
901	TCAAATAGTGGAGCAACTATGACATGCGCAAAACTTCTTAATGGAACGGT	950
317	lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps	334
951	TGTTCAAAAGCATCCAATGCCATGCCGTCACTTTGTGGATTAATCACGATT	1000
334	erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro	350
1001	CTCAACCTGGGAATCATTAGAATCATTTGTACAAGAAATGGTTTAGGCCA	1050
351	LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValph	367
1051	CTTGCTTATGCGCTATTTTAAACAGAGAACCAAGCTATCCCTCTGCTTT	1100
367	eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS	384
1101	CYATGTGACTACTATGGAAATCCAACACATAGTGTCCCAGCAATGAAAG	1150
384	erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr	400
:::::	:::::	
1151	CCAAGATTGATCCAATCTTAGAGCGCGCTCAAAATTTTGCATATGGAACA	1200
401	GlnHisAspTyrPheAspHisAspIleIleGlyTrpThrArgGluGl	417
1201	CACATGATTATTTTGACCATCATTAATATATCCGATGGACACGTCGAAG	1250
417	yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP	434
1251	AAATACCAGCATCCAATTCAGGACTTGGCACTATCATGTCGGATGGGC	1300
434	roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal	450
1301	CAGGGGGAGAGAAATGGATGTACGTAGGCGCAAAATAAAGCAGGTCAAGTT	1350
451	TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs	467
1351	TGGCATGACATAACTGGAAATAAACACGAGGAACATTCAGCATCAATGCCAGA	1400
467	pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL	484
1401	TGGATGGCTAAATTTTTTCAGTAAATGGAGGATCTGTTCCATTTGGGTGA	1450
484	ySgln 485	
451	AACGA 1455	



OM of: US-09-590-375-2 to: GenEmbl:\* out\_format : pfs

Date: Nov 28, 2001 6:27 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-O=/cgn2.1/uspto\_spool/US09590375/runat\_28112001.152037.21059/app\_query.fasta.1.1092  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500  
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0  
-MAXLEN=200000000 -USER=US09590375@cgn1.1.9071 -NCPU=6  
-ICPU=3 -LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPXY  
-WAIT -THREADS=1

Search information block:

Query: US-09-590-375-2  
Query length: 485  
Database: GenEmbl.\*  
Database sequences: 1472140  
Database length: -341344837  
Search time (sec): 2891.460000

score\_list:

Sequence	Strd Orig	zScore	E-Score	Len	Documentation
gb_pat:EI2445	+ 2713.00	3546.97	2.7e-189	1776	! EI2445 DNA encoding liquefacti
gb_ba:AB008763	+ 2713.00	3546.93	2.7e-189	1786	! AB008763 Bacillus sp. gene for
gb_pat:AR027254	+ 2613.00	3417.64	4.4e-182	1455	! AR027254 Sequence 4 from paten
gb_pat:AR049517	+ 2613.00	3417.64	4.4e-182	1455	! AR049517 Sequence 4 from paten
gb_pat:AR104348	+ 2613.00	3417.64	4.4e-182	1455	! AR104348 Sequence 4 from paten
gb_pat:AR129912	+ 2613.00	3417.64	4.4e-182	1455	! AR129912 Sequence 9 from paten
gb_pat:AR129917	+ 2613.00	3417.64	4.4e-182	1455	! AR129917 Sequence 14 from paten
gb_pat:AR137883	+ 2613.00	3417.64	4.4e-182	1455	! AR137883 Sequence 9 from paten
gb_pat:AR137887	+ 2613.00	3417.64	4.4e-182	1455	! AR137887 Sequence 13 from paten
gb_pat:AR143213	+ 2613.00	3417.64	4.4e-182	1455	! AR143213 Sequence 9 from paten
gb_pat:AR143217	+ 2613.00	3417.64	4.4e-182	1455	! AR143217 Sequence 13 from paten
gb_pat:AR087556	+ 2613.00	3417.63	4.4e-182	1458	! AR087556 Sequence 11 from paten
gb_pat:AR027255	+ 2400.00	3191.02	1.8e-169	1455	! AR027255 Sequence 5 from paten
gb_pat:AR049518	+ 2400.00	3191.02	1.8e-169	1455	! AR049518 Sequence 5 from paten
gb_pat:AR104349	+ 2400.00	3191.02	1.8e-169	1455	! AR104349 Sequence 5 from paten
gb_pat:AR129918	+ 2400.00	3191.02	1.8e-169	1455	! AR129918 Sequence 10 from paten
gb_pat:AR137884	+ 2400.00	3191.02	1.8e-169	1455	! AR137884 Sequence 15 from paten
gb_pat:AR137888	+ 2400.00	3191.02	1.8e-169	1455	! AR137888 Sequence 10 from paten
gb_pat:AR143214	+ 2400.00	3191.02	1.8e-169	1455	! AR143214 Sequence 14 from paten
gb_pat:AR143218	+ 2400.00	3191.02	1.8e-169	1455	! AR143218 Sequence 14 from paten
gb_ba:BSACMY66	+ 2409.00	3150.39	3.3e-167	1458	! MI8862 Bacillus sp. (alkalophil
gb_pat:AX036928	+ 2409.00	3150.39	3.3e-167	1458	! AX036928 Sequence 1 from paten
gb_pat:AX036930	+ 2409.00	3150.39	3.3e-167	1458	! AX036930 Sequence 3 from paten
gb_pat:AX037042	+ 2261.00	2956.52	2.1e-156	1458	! AX037042 Sequence 3 from paten
gb_pat:AX037040	+ 2256.00	2949.97	9.9e-156	1458	! AX037040 Sequence 1 from paten
gb_ba:AF220440	+ 1933.00	2249.76	4.9e-134	2160	! AF220440 Bacillus megaterium a
gb_ba:BSU22045	+ 1940.50	2532.32	8.9e-133	2470	! U22045 Bacillus sp. alpha-amyl
gb_pat:EI12201	+ 1912.00	2498.88	6.5e-131	1539	! EI12201 DNA encoding a heat-and
gb_pat:AR104350	+ 1910.50	2496.87	8.4e-131	1548	! AR104350 Sequence 6 from paten
gb_pat:AR129914	+ 1910.50	2496.87	8.4e-131	1548	! AR129914 Sequence 11 from paten
gb_pat:AR137885	+ 1910.50	2496.87	8.4e-131	1548	! AR137885 Sequence 11 from paten
gb_pat:AR143215	+ 1910.50	2496.87	8.4e-131	1548	! AR143215 Sequence 11 from paten
gb_pat:AX036894	+ 1910.50	2496.87	8.4e-131	1548	! AX036894 Sequence 7 from paten
gb_ba:BSAMYSGEN	+ 1910.50	2495.55	1.0e-130	1814	! X59476 B. stearothermophilus DN
gb_pat:AR008286	+ 1910.50	2495.55	1.0e-130	1814	! AR008286 Sequence 5 from paten
gb_pat:AR037276	+ 1910.50	2495.55	1.0e-130	1814	! AR037276 Sequence 5 from paten
gb_pat:AR052146	+ 1910.50	2495.55	1.0e-130	1814	! AR052146 Sequence 5 from paten
gb_pat:AR087552	+ 1910.50	2495.55	1.0e-130	1814	! AR087552 Sequence 5 from paten
gb_ba:AF032864	+ 1909.50	2493.46	1.3e-130	1990	! AF032864 Bacillus stearotherm

gb\_pat:A23402 + 1909.00 2495.46 1.0e-130 1449 ! A23402 B.licheniformis gene  
gb\_pat:A27772 + 1909.00 2495.46 1.0e-130 1449 ! A27772 Alpha amylase coding  
gb\_pat:A47677 + 1909.00 2494.95 1.1e-130 1539 ! A47677 Sequence 1 from Paté  
gb\_pat:AL17930 + 1909.00 2493.75 1.3e-130 1777 ! AL17930 Alpha amylase gene.  
gb\_pat:I24553 + 1909.00 2493.75 1.3e-130 1777 ! I24553 Sequence 33 from pat

seq\_name: gb\_pat:E12445

seq\_documentation\_block:  
LOCUS E12445 1776 bp DNA PAT 24-JUN-1998  
DEFINITION DNA encoding liquefaction type alkaline alpha amylase from Bacillus  
sp.  
E12445  
ACCESSION E12445  
VERSION E12445.1 GI:3251278  
KEYWORDS JP 1996336392-A/1.  
SOURCE Bacillus sp.  
ORGANISM Bacillus sp.  
Bacteria; Firmicutes; Bacillus/Clostridium group;  
Bacillus/Staphylococcus group; Bacillus.  
REFERENCE 1 (bases 1 to 1776)  
AUTHORS Hatada,Y., Ozaki,K., Ara,K., Kawai,S. and Ito,S..  
TITLE LIQUEFIED-TYPE ALKALI ALPHA-AMYLASE GENE  
JOURNAL Patent: JP 1996336392-A 1 24-DEC-1996;  
RAO CORP  
COMMENT OS Bacillus sp.  
PN JP 1996336392-A/1  
PD 24-DEC-1996  
PF 14-JUN-1995 JP 1995147257  
PI HATADA YUJI, OZAKI KATSUYA, ARA KATSUTOSHI, KAWAI SHUJI, PI  
ITO SUSUMU  
PC C12N15/09,C12N9/28;  
CC strandedness: Double;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No; Location/Qualifiers  
FH key  
FT source 1..1776  
FT /organism='Bacillus sp.'  
FT /strain='KSM-AP1378'  
FT /clone='pAML100'  
FT 5'UTR 1..144  
FT CDS 145..1695  
FT /product='Liquefaction type alkaline alpha FT  
FT amylase from  
FT Bacillus sp.'  
FT 3'UTR 1696..1776  
FT misc\_feature 1..31  
FT /note='Signal sequences'  
FT misc\_feature 127..132  
FT /note='SD sequences'  
FT -35\_signal 9..14  
FT -35\_signal 95..100  
FT -10\_signal 31..36  
FT -10\_signal 120..125.  
FEATURES  
Location/Qualifiers  
source 1..1776  
/organism='Bacillus sp.'  
/db\_xref='taxon:1409'  
BASE COUNT 575 a 305 c 417 g 479 t  
ORIGIN

alignment\_scores:  
Quality: 2713.00 Length: 485  
Ratio: 5.594 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000  
alignment\_block:  
US-09-590-375-2 x E12445 ..  
Align seg 1/1 to: E12445 from: 1 to: 1776

```

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
238 CATCAATAATGGGACGAATGGGACCATGATCAGTATTTTGAATGGCATTT 287
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
288 GCCAATATGACGGGAACCACTGGACAGGTTACGAGATGACGACGTAAC 337
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
338 TAAAGAGCTAAAGGATTAACCGCTGTTTGGATTCTCTCGCATGGAAGGG 387
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTrpAspLeuG 67
388 ACTTCGCAAAATGATGTGGGTATGGTATGCTATCATTTGTACGATCTGG 437
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
438 TGAGTTTAACCAAAAGGAACCGCTCGTACAAAATATGGCACAGGAGTC 487
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
488 AGTTGCAAGTGCCGTGACATCTTTGAAAAAATAACGGGATTCAAGTTAT 537
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
538 GGGGATGTCTGTATGAATCATAAAGGTGGACGACAGCGGACAGATGGT 587
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
588 AAATGCGGTGGAAGTGAACCGAAGCAACCGAAACCAAGAAATATCAGGTG 637
134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
638 AATPACACCATTTGAAGCATGGACGAAATTTGATTTCCTCGAAGAGGAAT 687
151 ThrHisSerAsnPheLysTrpArgTyrHisPheAspGlyThrAspTr 167
688 ACCATTCCAACTTAAATGGCGCTGGTATCATTTTGATGGGACAGATTG 737
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
738 GGATCAGTCACGTCAGCTTCAGAACAAAATATATAAATTCAGAGGTACCG 787
184 LyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTrpAspTr 200
788 GAAAGCATGGGACTGGGAAGTAGATATAGAACCGCAACTATGATTAC 837
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
838 CTATATGTCAGACATTCATGATGGATCCAGAAAGTAATCAATGAAC 887
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
888 TAGAAATGGGGAGTTGGTATACAAATACACTTAATCTAGATGGATTTA 937
234 rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
938 GAATCGATCTGTGAACATATTAATACAGCTATACGAGATTTGGCTA 987
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
988 ACACATGTCGTAACACCAACAGTAACCAATGTTGCAAGTTGCAGAA 1037
267 euTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284
1038 TTGGAAAAATGACCTTGCTGCAATCGAAACACTATTATAAATAAACAAGTT 1087
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTrpAsnAla 300
1088 GAATCACTCCGTGTCGATGTCCTCTTCATATAAATTTGTACAAATGCA 1137
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317

```

```

1138 TCCTAATAGTGGTGGCTATTTTGATATAGAAATATTTTAAATGGTTCGT 1187
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
1188 CGTACAAAACACCCCTATACATGCAGTCACATTTGTTGATAACCATGACT 1237
334 euGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
1238 CTCAGCCAGGAGAGCATTTGGAATCCTTTGTTCAATCGGTGTTCAACCA 1287
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
1288 CTGGCATATGCAATTGATTTCTGACAGGGAGCAAGGTTACCTTCCGTATT 1337
367 euTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
1338 TTACGGTGATTACTACGGTATACCAACTCATGTGTCTTCGATGAAAT 1387
384 euLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
1388 CTAAAATTGATCCACTTCTGAGGACAGTCAAACTGATCCCTACGGAACC 1437
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrTrpArgGluG 417
1438 CAACATGATTATTTGATCATCATGATATATATCGGCTGGACGAGAGAAG 1487
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
1488 GGACAGCTCCCAACCCAAATTCAGGACTTCGAACTATTTATGTCGGATGGG 1537
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
1538 CAGGGGGTAATAAATGGATGTATGCGGGAACATAAAGCTGGCCAAAGTA 1587
451 TrpArgAspIleThrClyAsnArgSerGlyThrValThrIleAsnAlaAs 467
1588 TGGAGAGATATCACCGGAAATAGGTCTGTGTACCGTCACCATTAATGCAGA 1637
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
1638 TGGTTGGGGGAATTCACATGTAACGAGGAGGCGCAGTTTCGGTTTGGTGA 1687
484 ysGln 485
1688 AGCAA 1692
seq_name: gb_ba:AB008763
seq_documentation_block:
LOCUS AB008763 1786 bp DNA BCT 21-AUG-1998
DEFINITION Bacillus sp. gene for amylase, complete cds.
ACCESSION AB008763
VERSION AB008763.1 GI:3445479
KEYWORDS amylase.
SOURCE Bacillus sp. (strain:KSM-1378) DNA.
ORGANISM Bacillus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
REFERENCE 1 (bases 1 to 1786)
AUTHORS Hatada,Y.
JOURNAL Direct Submission
Submitted (10-NOV-1997) to the DDBJ/EMBL/GenBank databases. Yuj1
Akabane, Ichikai, Haga-gun, Tochigi 321-3497, Japan
(Tel.:0285-68-7400, Fax:0285-68-7403)
REFERENCE 2 (bases 1 to 1786)
AUTHORS Igarashi,K., Hatada,Y., Ikawa,K., Araki,H., Ozawa,T., Kobayashi,T.,
Ozaki,K. and Ito,S.
TITLE Improved thermostability of a Bacillus alpha-amylase by deletion of
an arginine-glycine residue is caused by enhanced calcium binding
JOURNAL Biochem. Biophys. Res. Commun. 248 (2), 372-377 (1998)
MEDLINE 98342096

```

```

FEATURES
  source                Location/Qualifiers
  1..1786
    /organism="Bacillus sp."
    /strain="KSM-1378"
    /db_xref="taxon:1409"
  CDS
    155..1705
      /codon_start=1
      /transl_table=11
      /product="amylase"
      /protein_id="BAA32431.1"
      /db_xref="GI:3445480"
      /translation="MKLNRIISVLTLTLLAVAVLFPYMTPEQAQHHNNTNCTMIOYF
      EHLNPDNGNHNRLRDAANLKSGITAVIPPAWKGTSONDVGYGAYDLYDLGEFNQ
      KGTVRTKYGTSQLQAGAVTSLKNGNGIQVYGVVMNHKGGADGTEMVNAVEVNRSNRQ
      EISGEVTIEMTKFDPFGRGNTHSNFKRWYHFDGTDWDSROLQNKIKYKFRGTGKAW
      DWEVDIENGNDYDLAYADJMDHPVIELNRNKGWYNTNLNLDGFRIDAVKHIKYSY
      TDWLTHVRNTGKPMFAVEFKNDLAEINYLAKTSMNHSVDFVPLHYNLINASNS
      GYFDMRNILFNGSVOKHPIHATVFDVNDHDSQFGEALSFVQSWEFKPLAYAILLREQ
      GYPSVFYGDYIGIPHTGVPSMKSIDPLLAQRATVAYGTQHDYFDHHDIIIGTREGDS
      SHPNGLATIMSDPGGNKMYVGKHKAGQVWRDITGNRSQVTVINADGWGNTVNGG
      AVSVWVKQ"
  BASE COUNT          578 a 307 c 420 g 481 t
  ORIGIN
    alignment_scores:
      Quality: 2713.00      Length: 485
      Ratio: 5.594          Gaps: 0
      Percent Similarity: 100.000      Percent Identity: 100.000
    alignment_block:
      US-09-590-375-2 x AB008763 ..
      Align seg 1/1 to: AB008763 from: 1 to: 1786
      1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
      |||||
      248 CATCATATGGGAGCAATGGGACCATGATGCAGTATTTTGAATGGCAATT 297
      |||||
      17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
      |||||
      298 GCCAAATGACGGGACCACTGGAGACAGTTTACGAGATGACCGCACTAACT 347
      |||||
      34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
      |||||
      348 TAAAGAGTAAAGGATTAACCCCTGTTGGATTCTCTCGCATGGAAGGG 397
      |||||
      51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
      |||||
      398 ACTTCGCAAAATGATGTTGGGTATGGTGCCCTATGATTTGTACGATCTTGG 447
      |||||
      67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
      |||||
      448 TGAGTTTAACCAAGGGAACCGCCGTCACAAATATGGCAAGGAGTC 497
      |||||
      84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
      |||||
      498 AGTTGCAAGGTGCCGTGACATCTTTGAAATAATACGGGATTCAGTTTAT 547
      |||||
      101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
      |||||
      548 GGGGATGTCGTGATGAATCATATAAGGTGGAGCAGACGGGACAGAGATGGT 597
      |||||
      117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
      |||||
      598 AAATGCGGTGGAAGTGAACCGAAAGCAACCGAAACCAAGAAATATACAGGTG 647
      |||||
      134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyIleGlyAsn 150
      |||||
      648 ANTACACCATTTGAACCATGGACGAAATTTGATTTCCCTGGGAAGAGGAAT 697
      |||||
      151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
      |||||

```

```

698 ACCATTCCAACTTTAAATGGCGCTGGTGATCATTTTGTATGGACAGATTG 747
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
748 GGATCAGTCAGCTCAGCTTCAGAACAAAATATATAAATTCAGAGGTACCG 797
|||||
184 lYlYSAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
798 GAAAGGCATGGAGCTGGGAACTAGATATAGAGAACGGCAACTATGATTAC 847
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
848 CTTATGATGACAGCATTTGATATGATCATCCAGAAAGTAATCAATGAAT 897
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
898 TAGAAATGGGAGTTTGGTATACAAATACACTTAATCTAGATGATTTA 947
|||||
234 rGileAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
948 GAATCGATGCTGTGAAACATATTAATACAGTATACGAGAGATTGGCTA -997
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
998 ACATATGTCGCTAAACACACAGGTAAACCAATGTTTGCAGTTGCAGAA 1047
|||||
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
1048 TTGAAAATGACCTTGCTGCAATCGAAACATATTAAATAAACAAGTT 1097
|||||
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
1098 GGAATCACTCCGCTGTCGATGTCTCTCTTCAATTAATTTGTACAATGCA 1147
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
1148 TCTAATAGTGGTGCTATTTCATATGAGAAATATTTTAAATGGTCTGT 1197
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
1198 CGTACAAAACACCCCTATACATGACGTACATTTGTTGATTAACCATGACT 1247
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1248 CTCAGCCAGGAGAGCACTTGAATCCTTTGTTCAATCGTGGTTCAAACCA 1297
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1298 CTGGCATATGATTTGATTCACAAAGGAGCAAGGTTACCCCTCCGCTATT 1347
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
|||||
1348 TTACGGTGATTACTACGGTATACCAACTCATGGTGTTCCTTCGATGAAT 1397
|||||
384 erLysIleAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1398 CTAAATTTGATCCACTCTCTCAGGACGCTCAAACTGATGCCTACGGAACC 1447
|||||
401 GlnHisAspTyrPheAspHisHisAspIleGlyThrArgGluG 417
|||||
1448 CAACATGATTTATTTTATGATCATCATGATATATTCGGCTGGACGAGAGA 1497
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1498 GGACAGCTCCCAACCAATTCAGGACTTGCAACTATTATGTCGATGGGC 1547
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1548 CAGGGGGTAAATAATGGATGATGTGCGGAAACATAAAGCTGCGCCAAGTA 1597
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1598 TGGAGAGATATCACCGGAAATAGGTCTGTGTCACCGTCACCATTAATGCA 1647
|||||

```

467 pGlyTrpGlyAsnPhetHrValAsnGlyGlyAlaValSerValTrpValL 484  
 1648 TGGTTGGGGAAATTCACGTGTAACGGAGGCGCAGTTTCGGTTTGGGTGA 1697  
 484 ysGln 485  
 1698 AGCAA 1702

seq\_name: gb\_pat:AR027254

seq\_documentation\_block: 1455 bp DNA PAT 29-SEP-1999

LOCUS AR027254 Sequence 4 from patent US 5856164.

ACCESSION AR027254

VERSION AR027254.1 GI:5938094

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 1455)

AUTHORS Outtrup,H., Bisg,ang.rd-Frantzen,H., stergaard,P.Rahbek,

Rasmussen,M.Dolberg and Van Der Zee,P.

TITLE Alkaline bacillus amylase

JOURNAL Patent: US 5856164-A 4 05-JAN-1999;

FEATURES

Location/Qualifiers

1..1455

/organism="unknown"

BASE COUNT 461 a 248 c 361 g 385 t

ORIGIN

alignment\_scores:  
 Quality: 2613.00 Length: 485  
 Ratio: 5.421 Gaps: 0  
 Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AR027254 ..

Align seg 1/1 to: AR027254 from: 1 to: 1455

1 HishisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
 1 CATCATATGGAACAATGGTACTATGATGCAATATTTTCGAATGGTATT 50  
 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAsnL 34  
 51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGGATGACGACGTAAC 100  
 34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50  
 101 TAAAGATTAAGGATTAACAGCTGTATGGATCCACCTGCATGGAAGGG 150  
 51 ThrSerGlnAsnAspValGlyTyrGlyAlaValTrpAspLeuVal 67  
 151 ACTTCCAGAGATGATGAGTATGAGGCTATGATGATGATGATGATGATG 200  
 67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
 201 AGAGTTTAAACCAAGAGGCGGTCGTACAAATATGGAACACGCAACC 250  
 84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
 251 AGCTACAGGCTCGGTCGACCTCTTTAAAAAATAACGGCATTTTCAGGTAT 300  
 101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
 301 GGTGATGTCGTCATGAATCATTAAGGTTGGACGATGATGATGATGATG 350  
 117 IAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134  
 351 AAATCGGTAGAGTGAATCGGAGGACCGAACCGAAACCGAGGAG 400

134 luTyrThrIleGluAlaValTrpThrLysPheAspPheProGlyArgGlyAsn 150  
 401 AGTATGCAATAGACGCTGGACAAGTTGATTTCTCTGGAAGAGAAAT 450  
 151 ThrHisSerAsnPhelLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
 451 AACCATTCACGCTTTAAAGTGGCGCTGATCATTTTGATGGGACAGATTG 500  
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
 501 GGATCAGTCACCGCAGCTTCAAAACAAATATATAAATTCAGGGGAACAG 550  
 184 lLysAlaValTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
 551 GCARGGCTGGGACTGGGAAGTCGATACAGAGAAATGCAACATGACTAT 600  
 201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
 601 CTTATGTATGACAGCTGGATGGATGATGATGATGATGATGATGATGAT 650  
 217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
 651 TAGAACTGGGAGTGGTATACGATACACTGAACCTTGATGATTTA 700  
 234 tGlyLeuAspAlaValLysHisLysTyrSerTyrThrArgAspTrpLeu 250  
 701 GAATAGATGACGTGAACATATAAAATATAGCTTTACGAGAGATTGGCTT 750  
 251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
 751 ACACATGTGCGTAACACACACAGGTAAACCAATGTTGCGAGTGGCTGAG 800  
 267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
 801 TTGGAAAAATGACCTGGTGGCAATTTGAAACATATTGAAATAAAACAGTT 850  
 284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
 851 GGAATCACCTCGGTGTGATGTTCTCTCCACTATAAATTTGTACAATGCA 900  
 301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
 901 TCTAATAGCGGTGGTATTATGATGATGAGAAATATTTTAAATGGTCTGT 950  
 317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334  
 951 GGTGCAAAACATCCACACATGCCGTTACTTTTGTGATAACCATGATT 1000  
 334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
 1001 CTCAGCCCGGGGAAGCATTTGGAATCCTTTGTTGATAACCATGATT 1050  
 351 LeuAlaValAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
 1051 CTTGCATATGATGCTTCTCTGACAGGGAACAAGTTATCTCTCCGTATT 1100  
 367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384  
 1101 TTTATGGGATTTACTACGGTATCCCAACCCATGGTGTTCGGCTATGAAAT 1150  
 384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaValTyrGlyThr 400  
 1151 CTAAATAGACCTCTTCTCAGGACGCTCAAACTTTTGGCTATGTTAGC 1200  
 401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417  
 1201 CAGCATGATTACTTTGATCATCATGATATATCGTTGGACAGAGAGGG 1250  
 417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
 1251 AAATAGTCCCATCCAAATTCAGGCCCTTGCACCATTTATGTCAGATGCTC 1300

434 rGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
 1301 CAGGTGGTAAACAAATGGATGATGTGGGAAATAAAGCGGCAAGTT 1350  
 451 TrpArgSpilleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
 1351 TGGAGAGATATATCCGGAATAGACAGGCCCGCTCACAATTAATGCAGA 1400  
 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
 1401 CGGATGGGTAAATTCCTCTGTTAATGGAGGTCGTTTCGGTTGGGTGA 1450  
 484 ySgIn 485  
 1451 AGCAA 1455

seq\_name: gb\_pat:AR049517

seq\_documentation\_block: AR049517 1455 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 4 from patent US 5824531.

ACCESSION AR049517

VERSION AR049517.1 GI:6005556

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE Rasmussen, M. Dolberg and Van der Zee, P.

JOURNAL Alkaline bacillus amylase

FEATURES Patent: US 5824531-A 4 20-OCT-1998;

Location/Qualifiers

1..1455

Source

BASE COUNT 461 a 248 c 361 g 385 t

ORIGIN

alignment\_scores:

Quality: 2613.00 Length: 485

Ratio: 5.421 Gaps: 0

Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AR049517 ..

Align seg 1/1 to: AR049517 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17

1 CATCATATGGAACAAATGGTACTATGATGCAATATTTTCAATGGTATT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34

51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGATGACGACGCTAACT 100

34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50

101 TAAAGAGTAAAGGGATACACGCTGTATGGATCCCACTTCGATGGAAGGG 150

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG1 67

151 ACTTCCCAAGATGATAGGTATGAGCCCTATGATTTATATGATCTTGG 200

67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84

201 AGAGTTTAAACAGAGGGGCGGTTTCGTACAAAATATGGAACACGCAACC 250

84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100

251 AGCTACAGGCTGCGGTGACCTCTTTAAAAAATAACGGCATTCAGGTATAT 300

101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
 301 GGTGATGCTGTCATGAATCAATAAGGTGGACGACATGGTACGGAATTTGT 350  
 117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
 351 AAATCGCGGTAGAGTGAATCGGAGCAACCGAAACGAGGAAACCTCAGGAG 400  
 134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
 401 AGTATGCAATAGAACGGTGGACAAGTTTGATTTTCCTGGAGAGGAAAT 450  
 151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
 451 AACCATCCAGCTTTAAGTGGCGTGGTATCATTTTGTATGGACAGATTG 500  
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
 501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGACAG 550  
 184 lLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
 551 GCAAGGCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600  
 201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
 601 CTTATGATGCAGCGTGGATATGGATCACCAGCAAGTAATACATGAAC 650  
 217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
 651 TAGAACTGGGAGTGTGGTATACGAATACACTGAACCTTGATGATTTA 700  
 234 rgIleAspAlaValLysHisLysTyrSerTyrThrArgAspTrpLeu 250  
 701 GAATAGATGCAGTGAACATATAAATATAGCTTTTACGAGAGATTTGGCT 750  
 251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
 751 ACACATGTGCGTAAACACACAGGTAACCAATGTTTTCAGTGGCTGACT 800  
 267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSert 284  
 801 TTGGAAAAATGACCTTGGTGCATTTGAAACATATTTTGAATAAACCAAG 850  
 284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
 851 GGAATCAGCTCGGTGTGATGTTCTCTCCACTATAATTTGTACAAATGCA 900  
 301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
 901 TCTAATAGCGTGGTTATATGATATGAGAAATATTTTAAATGGTTCGT 950  
 317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
 951 GGTGCAAAACATCCACACATGCGGTACTTTTGTGATTAACCATGATT 1000  
 334 erGlnProGlyGluAlaLeuSerPheValGlnSerTrpPheLysPro 350  
 1001 CTCAGCCCGGGGAAGCATTTGGAATCTTTTGTTCACAAATGGTTAAACCA 1050  
 351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
 1051 CTTGCATATGATTTGGTCTGCACAGGGAACAGGTTATCTTCCGTATT 1100  
 367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384  
 1101 TTATGGGATTAACGATACGATCCCAACCATGCGTGTTCGCGCTATGAAT 1150  
 384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
 1151 CTAAATAGACCCCTCTCTCGAGGACGCTCAAACTTTTGCCTATGGTACG 1200  
 401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG1 417

```

|||||
1201 CACGATGATTACCTTTGATCATCATGATATTATCGGTTGGACAAGAGGG 1250
417 YASPSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGCTCCCATCCAAATTCAGCGCTTGCACCATATATGTCAGATGGTC 1300
434 roGlyGlyAsnLysTrpMetYrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGGTAAACAAATGATGATGTGGGAAAAATAAAGCGGACAAAGTT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATTACCGGAATAGCAGGACCGCTCACAAATTAATCGAGA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
|||||
1401 CGGATGGGTAATTTCTCTGTTAATGAGGTCGGTTTCGGTTTGGGTGA 1450
484 ySgln 485
|||||
1451 AGCAA 1455

```

seq\_name: gb\_pat:AR104348

seq\_documentation\_block: 1455 bp DNA PAT 14-FEB-2001

LOCUS AR104348 Sequence 4 from patent US 6093562.

DEFINITION AR104348

ACCESSION AR104348

VERSION AR104348.1 GI:12817056

KEYWORDS

SOURCE unknown.

ORGANISM unknown.

REFERENCE 1 (bases 1 to 1455)

AUTHORS Bisq.ang.rd-Prantzen,H., Svendsen,A. and Borchert,T.Vedel.

TITLE Amylase variants

JOURNAL Patent: US 6093562-A 4 25-JUL-2000;

FEATURES Location/Qualifiers

1..1455

/organism="unknown"

BASE COUNT 461 a 248 c 361 g 385 t

ORIGIN

alignment\_scores:

Quality: 2613.00 Length: 485

Ratio: 5.421 Gaps: 0

Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AR104348 ..

Align seg 1/1 to: AR104348 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17

1 CATCATTAATGGAACAATAATGGTACTATGATGCAATATTTCCAAATGGTATT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34

51 GCCAATGACGGGAATCATGTGACAGGTTGAGGGATGACGAGCTTAAT 100

34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50

101 TAAAGAGTAAAGGATAACAGCTGTATGATCCACCTGCATGGAAGGG 150

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67

151 ACTTCCCAAGATCATGTAGTATGAGGCTATGATTTATATCATCTGG 200

67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

```

201 AGAGTTTAAACCAGAGGGGACGGTTCGTCAAAAATATGGAACACGCAACC 250
84 InLeuGlnGlyAlaValThrSerLeuLysAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGCTGGGTGACCTCTTTAAAAAATAACGGCAATTCAGGTATAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCTCATGAATCATAAAGGTGGACGAGATGGTACGGAATTCG 350
117 IAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351 AAATCGGTTAGAGTGAATCGGAGCAACCCAGAAACCCAGGAACCTCAGGAG 400
134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGACGGTGGACAAAGTTTGATTTCTCGAAGAGGAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTCACAGCTTAAAGTGGCGCTGGTATCATTTTGATGGGACAGATTG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACCCGACCTTCAAAAACAAAATATATAAATTCAGGGGAACAG 550
184 LyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAGGCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATCTATGCAGACGTGGATATGGATCACCAGAAAGTAATACATGAAC 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTCGGGAGTGGTATACGAATACACTGAACCTTGATGGATTTA 700
234 rGileAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGCACCTGAAACATATAAATATAGCTTTACGAGAGATGGCTT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGCGTAACACCACAGGTAAACCAATGTTTGCAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSer 284
|||||
801 TTGGAATAATGACCTTGGTGGCAATTTGAAACACTATTGTAATAAACAA 850
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCAGCTCGGTGTTGATGTTCTCTCCACTATAAATTTGTACAAATG 900
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGTTATATGATGATGAGAAATATTTAAATGGTTCGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTGCAAAACATCCACACATGCGCGTTACTTTTGTGATAACCATGATT 1000
334 exGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCACCCCGGGGAACCATTTGGAATCCTTTGTTCACAATGGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValph 367
|||||
1051 CTTGATATGATGTTGTTCTGACAAAGGAAACAAAGGTATATCTCTCCGTAT 1100
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384
|||||
1101 TTATGGGATTAATACTACGGTATCCCAACCCATGGTGTTCGGCTATGAAT 1150

```

384 erLysIleAspProLeuLeuGlnAlaArgGlnThrThrAlaTyrGlyThr 400  
 1151 CTAAGATAGACCCCTCTCTGCAGCACGCTCAAACTTTTGGCTATGGTACG 1200  
 401 GlnHisAspTyrPheAspHisHisAspIleleGlyTrpThrArgGluG1 417  
 1201 CAGCATGATTACTTTGATCATCATCATATTATCGGTTGGACAAGAGGG 1250  
 417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSeraspGlyP 434  
 1251 AAATAGCTCCCATCAAAATTCAGGCCCTTGCACCATTATGTCAGATGTC 1300  
 434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
 1301 CAGGTGGTAACAAATGGATGTATGTGGGAAATAAAGCGGGACAAGTT 1350  
 451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
 1351 TGGAGAGATATTACCGGAATAGGACAGGCACCGTCACAATTAATGCAGA 1400  
 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValaSerValTrpValL 484  
 1401 CGGATGGGGTAATTCTCTGTAAATGGAGGTCGCTTCGGTTGGGTGA 1450  
 484 ysGln 485  
 1451 AGCAA 1455

seq\_name: gb\_pat:AR129912

seq\_documentation\_block: 1455 bp DNA PAT 16-MAY-2001  
 LOCUS AR129912  
 DEFINITION Sequence 9 from patent US 6187576.

ACCESSION AR129912

VERSION AR129912.1 GI:14117809

KEYWORDS

SOURCE

ORGANISM

Unclassified

REFERENCE 1 (bases 1 to 1455)

AUTHORS Svendsen,A., Borchert,T.Vedel and Bisg.ang.rd-Frantzen,H.

TITLE .alpha.-amylase mutants

JOURNAL Patent: US 6187576-A 9 13-FEB-2001;

FEATURES

source 1..1455

/organism="unknown"

BASE COUNT 461 a 248 c 361 g 385 t

ORIGIN

alignment\_scores:

Quality: 2613.00 Length: 485

Ratio: 5.421 Gaps: 0

Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AR129912

Align seg 1/1 to: AR129912 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17

1 CATCATATGGACAAATGGTACTATGATGCAATATTTGCAATGGTATT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34

51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGATGACGACGCTAACT 100

34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50

101 TAAAGAGTAAAGGGGATAACAGCTGTATGGATCCCACTGCATGGAAGGG 150

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG1 67  
 151 ACTTCCCAAGAAATGATGATAGTTATGGAGCCTATGATTTATATGATCTGG 200  
 67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
 201 AGAGTTTAAACAGAGAGGGGACGTTCTGTACAAAATATGGAACACGCAACC 250  
 84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
 251 AGCTACAGCGTGGCTGACCTTTTAAAAAATAACGGCATTTCAGGTATAT 300  
 101 GlyAspValValMetAsnHisLysGlyAlaAspGlyThrGluMetVa 117  
 301 GGTGATGTCGTCATCAATCAATAAGGTGGAGCAGATGTCACGGAATTTGT 350  
 117 lasAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
 351 AAATCGCGGTAGAAAGTGAATCGGAGCAACCGAAACCCAGGAAACCTCAGGAG 400  
 134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
 401 AGTATGCAATAGAACGCTGGACAAGTTTGATTTTCTGGAGAGGAAAT 450  
 151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
 451 AACCATTCAGCTTTAAGTGGCGCTGGTATCATTTTGTATGGACAGATTG 500  
 167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
 501 GGATCAGTCAGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550  
 184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
 551 GCAAGGCTGGGACTGGGAAGTCGATACAGAGAAATGGCAACTATGACTAT 600  
 201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
 601 CTTATGATGCAGAGCTGGATATGGATCACCAGAAAGTAATACATGAAC 650  
 217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
 651 TAGAAACCTGGGAGCTGTGTATACGAATACATCAACCTTGTATGATTTA 700  
 234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
 701 GAATAGATGCAGTGAACATATATAAATATAGCTTTACGAGAGATGGCTT 750  
 251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
 751 ACACATGTGCGTAAACACACACAGGTAACCAATGTTTGCAGTGGCTGACT 800  
 267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSert 284  
 801 TTGCAAAAATGACCTTGTGTCAATTTGAAACCTATTTTGAATAAACAAGTT 850  
 284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
 851 GGAATCACTCGGTGTTGATGTCTCTCCACATATAATTTGTACAAATGCA 900  
 301 SerAsnSerGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
 901 TCTAATACCGGTGGTTATTCATGATGAGAAATATTTTAAATGGTCTGT 950  
 317 lvaGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
 951 GGTGCAAAAACATCCACACATCGCGTTACTTTTGTGTATAACCATGATT 1000  
 334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPhelysPro 350  
 1001 CTCAGCCCGGGGAGCATTGGAAATCCTTTGTTCACAACATGGTTTAAACCA 1050  
 351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367

```

|||||
1051 CTTGCATATGCTTGGTCTGACAGGGAACAAGCTTATCCTTCGCTATT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
|||||
1101 TTATGGGATTACTACGGGTATCCCAACCCATGGTTCGGGCTATGAAAT 1150
|||||
384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAAATAGACCCTCTTCGACGGCACGTCAAACCTTTGGCCTATGGTACG 1200
|||||
401 GlnHisAspTyrPheAspHisAspIleIleGlyTrpThrArgGluGI 417
|||||
1201 CAGCATGATTACTTTCATCATCATGATATATCGGTGGACAAGAGAGGG 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGCTCCCAATTCAGGCTTGGCCACCATATATGTGAGATGGTC 1300
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGGTAAACAAATGGATGTATGGGAAAAAATAAAGCGGACAAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATTACCGAAATAGGACAGGCACCGTCACAATTAATGCAGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
|||||
1401 CGGATGGGTAATTTCTCTGTTAATGGAGGGTCCGTTTCGGTTTGGGTGA 1450
484 ysgln 485
|||||
1451 AGCAA 1455

```

seq\_name: gb\_pat:AR129917

```

seq_documentation_block:
LOCUS AR129917 1455 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 14 from patent US 6187576.
ACCESSION AR129917
VERSION AR129917.1 GI:14117814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1455)
AUTHORS Svendsen,A., Borchert,T.Vedel and Bisg.ang.rd-Frantzen,H.
TITLE - .alpha.-amylase mutants
JOURNAL Patent: US 6187576-A 14 13-FEB-2001;
FEATURES
Location/Qualifiers
source
1..1455
/organism="unknown"
BASE COUNT 461 a 248 c 361 g 385 t
ORIGIN

```

alignment\_scores:  
Quality: 2613.00 Length: 485  
Ratio: 5.421 Gaps: 0  
Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AR129917 ..

Align seg 1/1 to: AR129917 from: 1 to: 1455

```

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGlnTrpHisLe 17
|||||
1 CATCAATAGGACAAATGGTACTATGATGCAATATTTCCGAATGGTATT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34
|||||

```

```

51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGATGACCGAGCTAACT 100
34 euLysSerLysGlyIleThrAlaValTTPileProAlaTrpLysGly 50
|||||
101 TAAGAGTAAAGGATAACACCTGTATGGATCCACCTGCATGGAAGGG 150
|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGI 67
|||||
151 ACTTCCCAAGAAATGATGTAGGTTATGGAGCCTATGATTTATATGATCTTGG 200
|||||
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACAGAGGGGACGGTTCTGACAAAATATGGAACACCAACC 250
|||||
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGCTGCGGTGACCTCTTTAAAAAATAACGGCATTTCAGGTATAT 300
|||||
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCGTCAATGAATCATAAAGTGGAGCAGATGGTACGGAATTTGT 350
|||||
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGlnIleSerGlyG 134
|||||
351 AAATCCGGTAGAAGTGAATCGGAGCAACCGAAACCGAAGAACTTCAGGAG 400
|||||
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAACGCTGGACAAAGTTTGATTTTCTGGAAGAGGAAT 450
|||||
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTCAGCTTTAAGTGGCGCTGGTATCATTTTGATGGGACAGATTG 500
|||||
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACGCCAGCTCAAAACAAATAATATAAATTCAGGGGAACAG 550
|||||
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGGCTCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGTATGCAGACGTGGATATGGATCACCCAGAGATTAATACATGAAC 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAACTGGGAGTGTGTATACGAATACACTGAACCTTGATGGATTTA 700
|||||
234 rgLleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATCAGTGAACATATAAAATATAGCTTTACGAGAGATTGGCTT 750
|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTCGTTAACACACACAGGTAACCAATGTTTGCAGTGGCTGAGTT 800
|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
|||||
801 TTGGAAAAATGACCTTGGTGCATTTGAAACTATTTGAAATAAAACAAGTT 850
|||||
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCAGTCGGGTGTGATGTTCTCTCCATATTAATTTGTACAAATGCA 900
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATAGCGGTGGTTATTATGATATAGAAAATATTTTAAATGGTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334
|||||
951 GGTGCAAAAACATCCCAACACATGCCGTTACTTTTGTGTGATACCATGATT 1000

```



334 exGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
|||||  
1001 CTCACCGCGGGAACATCGAATCTTGTTCACAAATGGTTTAAACCA 1050  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
|||||  
1051 CTTGCATATGCAATGGTCTCAGCAAGGAACAAAGGTTATCCTTCGGTAT 1100  
367 eYrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384  
|||||  
1101 TTATGGGATTAACGTACTACGGTATCCCAACCCATGGTTCGGGTATGAAT 1150  
384 exLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
|||||  
1151 CTAAATAGACCCCTCTCTCGAGGACGCTCAAACTTTGGCTATGGTACG 1200  
401 GlnHisAspTyrPheAspHisHisAspIleLeuGlyTyrThrArgGluG 417  
|||||  
1201 CAGCATGATTAATCTGTATCATCATATATATCGGTTGGCAAGAGAGGG 1250  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
|||||  
1251 AAATAGCTCCCATCAATTCAGGCTTGGCCACCAATATATGATGATGGTC 1300  
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
|||||  
1301 CAGGTGGTAACAAATGGATGATGTGGGAAATAAAGCGGACAAAGTT 1350  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
|||||  
1351 TGGAGAGATATATACCGGAATAGGACAGCCGTCACAAATTAATGSCAGA 1400  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
|||||  
1401 CGATGGGGTAATTTCTCTGTTAATGGAGGGTCGCTTTCCGGTTGGGTGA 1450  
484 ysGln 485  
|||||  
1451 AGCAA 1455

seq\_name: gb\_pat:AR137883

seq\_documentation\_block: 1455 bp DNA PAT 16-JUN-2001  
LOCUS AR137883  
DEFINITION Sequence 9 from patent US 6197565.  
ACCESSION AR137883  
VERSION AR137883.1 GI:14479392

KEYWORDS  
SOURCE  
ORGANISM

Unclassified.

REFERENCE  
1 (bases 1 to 1455)  
AUTHORS Svendsen,A., Kjaerulf,S., Bisgaard-Frantzen,H. and Andersen,C.  
TITLE .alpha.-Amylase variants  
JOURNAL Patent: US 6197565-A 9 06-MAR-2001;  
FEATURES  
source  
1. 1455  
Location/Qualifiers

BASE COUNT 461 a 248 c 361 g 385 t

ORIGIN

alignment\_scores:

Quality: 2613.00 Length: 485  
Ratio: 5.421 Gaps: 0  
Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-09-590-375-2 x AR137883 ..

Align seg 1/1 to: AR137883 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
|||||  
1 CATCATATGAACAAATGGTACTATGATGCAATATTTCGAATGCTATT 50  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34  
|||||  
51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGATGACGAGCTAACT 100  
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50  
|||||  
101 TAAAGAGTAAAGGGATAACAGCTGTATGATCCCACTGCATGGGAAGGG 150  
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67  
|||||  
151 ACTTCCCAAGATGATGATAGGTATGAGCCATGATTTATATGATCTGG 200  
67 yClnPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
|||||  
201 AGAGTTTAAACCAAGAGGGGCGGTTTCGTACAAAATATGGAACACCAACC 250  
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
|||||  
251 AGCTACAGCTGCGGTGACCTCTTTAAATAATAACGGCATTCAGGTATAT 300  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||  
301 GGTGATGTCGTATCATCAATCAATAAAGTGGAGCAGATGTTACGGAATGT 350  
117 IasnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
|||||  
351 AAATCGGTAGAAAGTGAATCGGAGCAACCGAAACCCAGGAACCTCAGGAG 400  
134 LuTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
|||||  
401 AGTATGCAATAGAACCGTGGACAAAGTTTGATTTCTCTGGAAGAGAAAT 450  
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
|||||  
451 AACCATTCAGCTTTAAGTGGCGCTGGTATCATTTTGTGGGACAGATTG 500  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
|||||  
501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550  
184 LyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
|||||  
551 GCAAGCGCTGGGACTGGGAAGTCGATACAGAATGGCAACTATGACTAT 600  
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
|||||  
601 CTTATGTATGCAGACGTGGATATGGATCACCAGAAAGTAATACATGAAC 650  
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
|||||  
651 TAGAAACTGGGAGTGGTGTATACGAATACACTGAACCTTGATGATTGA 700  
234 rgIleAspAlaValLysHisLysTyrSerTyrThrArgAspTrpLeu 250  
|||||  
701 GAATAGATGCAGTGAACATATATAAATATAGCTTTACGAGAGATTCGCT 750  
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
|||||  
751 ACACATGTGCGTAAACACACACAGGTAACCAATGTTTGCAGTGGCTGAGTT 800  
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSert 284  
|||||  
801 TTGGAAAAATGACCTTGGTGTCAATTTGAAACATATTGTAATAAACAACT 850  
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
|||||  
851 GGAATCACCTCGGTGTTGATGTTCTCTCCACTATAATTTGTACANTGCA 900  
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317

```
|||||
901 TCFAATAGCGGTGGTATTATGATATGAGAAATATTTAAATGGTTCTGT 950
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||
951 GGTGCAAAACATCCACACATCCGCTACTTTGTTGATAACCAATGATT 1000
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAGCCCGGGGAAGCATTTGGAATCTCTTTGTTCAACAATGGTTTAAACCA 1050
351 LeuAlaTyrAlaLeuLeuLeuThrArgGluGlnGlyTyrProSerValph 367
|||||
1051 CTTGCATATGCAATGGTCTGACAAAGGGAACAAAGGTTATCTCTCCGTATT 1100
367 eTyrGlyAspTyrTyrGlyLeuProThrHisGlyValProSerMetLys 384
|||||
1101 TTATGGGGATTACTAGGTATCCCAACCCATGGTCTCCGGCTATGAAT 1150
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAAATAGACCTCTCTGCGAGGACGTCAAACTTTTGCTATGTGTACG 1200
401 GlnHisAspTyrPheAspHisAspIleIleGlyTrpThrArgGlu 417
|||||
1201 CAGCATGATTACTTTGATCATCATGATATATCGGTGGACAGAGAGGG 1250
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AATAGCTCCCATCCAAATTCAGGCCCTTCCACCAATATGTCTAGATGGTC 1300
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGGTGGTAACAAATGGATGTATGTGGGAAAAATAAAGCGGACAAATT 1350
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATTACCGGAATAGGACAGGACCGGTCCACAAATTAATCGA 1400
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484
|||||
1401 CGGATGGGTAAATTTCTCTGTTAATGGAGGTCCTGTTTCGGTTGGGTGA 1450
484 ysgln 485
1451 ACAA 1455
```

seq\_name: gb\_pat:ARL37887

```
seq_documentation_block: 1455 bp DNA PAT 16-JUN-2001
LOCUS ARL37887
DEFINITION Sequence 13 from patent US 6197565.
ACCESSION ARL37887
VERSION ARL37887.1 GI:14479396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1455)
AUTHORS Svendsen,A., Kjaerluff,S., Bisgaard-Frantzen,H. and Andersen,C.
TITLE .alpha.-Amylase variants
JOURNAL Patent: US 6197565-A 13 06-MAR-2001;
FEATURES
source
location/Qualifiers
1..1455
/organism="unknown"
BASE COUNT 461 a 248 c 361 g 385 t
ORIGIN
```

alignment\_scores:

```
Quality: 2613.00 Length: 485
Ratio: 5.421 Gaps: 0
Percent Similarity: 99.381 Percent Identity: 95.052
```

alignment\_block:

US-09-590-375-2 x ARL37887

Align seg 1/1 to: ARL37887 from: 1 to: 1455

```
1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCATAAATGGAACAATGGTACTATGATGCAATATTTGGAATGGTATT 50
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
|||||
51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGGATGACGCACTAAC 100
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
|||||
101 TAAAGAGTAAAGGATAACAGCTGTATGGATCCACCTGCATGGAAGGG 150
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
|||||
151 ACTTCCCAAGATCATGTAGGTTATGGAGCCTATGATTTATATGATCTTG 200
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGGGGACGGTTGCTACAAAATATGGAACACGCAAC 250
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGCTCGGTGACCTCTTTAAAAAATAACGGCAATTCAGGTAT 300
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGCTCATGAATCATAAAGGTGGAGCAGATGTTACGGAATTTGT 350
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134
|||||
351 AAATCGGTAGAGTGAATCGGAGCAACCGAAACCCAGAAACCTCAGGAG 400
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 ACTATGCAATAGACGCTGGACAAAGTTTGATTTCTCGAAGAGGAAT 450
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTCACGCTTAAAGTGGCGCTGGTATCATTTTGTGGGACAGATTG 500
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
184 lYlYAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGCCCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluTe 217
|||||
601 CTTATGTATGCAGACGTGGATATGGATCACCAGAAAGTAATACATGAAC 650
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAACTGGGAGTGTGGTATACGAATACACTGAACCTTGATGGATTTA 700
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGCACTGAAACATATAAAATATAGCTTTACGAGAGATTGGCT 750
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||
751 ACACATGTGCGTAACACCAAGGTAACCAATGTTTGCAGTGGCTGAGTT 800
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284
|||||
801 TTGGAAAAATGACCTTGGTGCATTTGAAACACTATTGTAATAAACAAAGT 850
```

```
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||
851 GGAATCACTCGGTTCATGCTTCTCCACTATATTTGTACAATGCA 900
|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||
901 TCTAATACGGTGGTATATGATGATGAGAAATATTTAAATGGTCTGT 950
|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 334
|||||
951 GGTGCAAAACATCCACACATGCCGTACTTTTGTGATAACCATGATT 1000
|||||
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
|||||
1001 CTCAGCCCGGGGAGCATGGAATCCCTTGTTCACAATGCTTTAAACCA 1050
|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||
1051 CTTGCATATGCTTGGTTCGACAAAGGGAACAAGTTATCTCCGTATT 1100
|||||
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
|||||
1101 TTATGGGATTAACGCTATCCCAACCCATGGTTCGGGCTATGAAT 1150
|||||
384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||
1151 CTAAATAGACCTCTCTCGAGCAGCTCAAACTTTTGCCATATGGTACG 1200
|||||
401 GlnHisAspTyrPheAspHisHisAspIleLeGlyTrpThrArgGluGl 417
|||||
1201 CAGCATGATTACTTTGATCATCATGATATATTCGTTGGCAAGAGAGGG 1250
|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||
1251 AAATAGCTCCCATCAAAATCAGGCCCTTGCCACCATTATGTCAGATGTC 1300
|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||
1301 CAGCTGTAACAATGGATGATGTCGGGAAATAAAGCGGACAAAGTT 1350
|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||
1351 TGGAGAGATATATACCGAAATPAGACAGGACCCTCACAAATTAATGAGA 1400
|||||
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
|||||
1401 CGGATGGGGTAATTTCTGTGTAATGAGGGTCCGTTTCGGTTTGGGTGA 1450
|||||
484 ySgIn 485
|||||
1451 AGCAA 1455

seq_name: 9b_pat:ARI43213

seq_documentation_block:
LOCUS   ARI43213      1455 bp      DNA              PAT      08-AUG-2001
DEFINITION   Sequence 9 from patent US 6204232.
ACCESSION   ARI43213
VERSION     ARI43213.1  GI:15104499
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1455)
AUTHORS    Borcherdt,T,Vedel, Svendsen,A., Andersen,C., Nielsen,B.,
            Nissen,T.Lauesgaard and Kj.ae buttet.ruliff,Sslashedren.
TITLE       .alpha.-amylase mutants
JOURNAL    Patent: US 6204232-A 9 20-MAR-2001;
FEATURES
            Location/Qualifiers
            1..1455
            /organism="unknown"
BASE COUNT  461 a  248 c  361 g  385 t
```

## ORIGIN

```
alignment_scores:
Quality: 2613.00      Length: 485
Ratio: 5.421          Gaps: 0
Percent Similarity: 99.381  Percent Identity: 95.052

alignment_block:
US-09-590-375-2 x ARI43213
..
Align seg 1/1 to: ARI43213 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||
1 CATCATATATGGAACAATGGTACTATGATGCAATATTTTCCGAATGGTATT 50
|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
|||||
51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGATGACGCAGCTAACT 100
|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50
|||||
101 TAAAGAGTAAAGGATAACAGCTGTATGGATCCCACTTCATGGAAGGGG 150
|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl 67
|||||
151 ACTTCCCAAGAATGATGATAGGTATGAGGCCATGATTTATATGATCTTGG 200
|||||
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||
201 AGAGTTTAAACCAAGAGGGGCGGTTTCGTACAAATATATGGAACACGCAAC 250
|||||
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||
251 AGCTACAGGCTGCGGTGACCTCTTTTAAAAAATAACGGCATTTCAGGTATAT 300
|||||
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||
301 GGTGATGTCGTCATGAATCATAAAGGTGGAGCAGATGGTACGGAATTTGT 350
|||||
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||
351 AAATGCGGTAGAAAGTGAATCGGACCAACCGAAACAGGAAACCTCAGGAG 400
|||||
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
|||||
401 AGTATGCAATAGAACCGTGGACAAAGTTTGATTTTCTTGSAAAGAGAAAT 450
|||||
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
|||||
451 AACCATTTCCAGCTTTAAGTGGCGTGGTATCATTTTGTATGGACAGATTG 500
|||||
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||
501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550
|||||
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||
551 GCAAGGCCCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600
|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||
601 CTTATGATGACAGCGTGGATATGGATCACCACAGAAATATACATGAACT 650
|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||
651 TAGAAACTGGGAGTGTGTTATACGAATACACACTGAACCTTGATGATTTA 700
|||||
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||
701 GAATAGATGCAGTGAACATATAAAATATAGCTTTTACGAGAGATTGGCTT 750
```

251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
|||||  
751 ACACATGTGCGTAACACACACAGTAACCAATGTTTGCAGTGGCTGAGTT 800  
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSert 284  
|||||  
801 TTGGAAAATGACCTTGGTGGCAATTTGAAACTATTGTAATAAACAAAGTT 850  
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
851 GGAATCACTCGGTGTTGATGCTCTCCACTATAAATTTGACAAATGCA 900  
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
901 TCTAATAGCGGTGGTTATTATGATATGAGAAATATTTAAATGGTTCTGT 950  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
951 GGTGCAAAAACATCCCAACACATGCGGTTACTTTTGTGATAACCATGATT 1000  
334 exGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
1001 CTCAGCCCGGGAGCATTTGGAACTCTTTGTTCAACAATGGTTAAACCA 1050  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValph 367  
1051 CTTGCATATGCATTGGTCTGACAAAGGAACAAGGTTATCTCTTCGGTATT 1100  
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384  
1101 TTATGGGGATTACTAGGGTATCCCAACCCATGGTGTTCGGGTATGAAAT 1150  
384 eTylsIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
1151 CTAAATACACCTCTCTCAGGCACGTCAAACITTTTGCCTATGGTAGC 1200  
401 GlnHisAspTyrPheAspHisAspIleIleGlyTyrTrpArgGluGl 417  
1201 CAGCATGATTACTTTGATCATCATGATATATATCGGTGGGACAGAGGG 1250  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyp 434  
1251 AAATAGCTCCCATCCAAATTCAGGCCCTGCCACCATATATGTCAGATGGTC 1300  
434 rGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
1301 CAGGTGTAACAAATGCATGTATGTGGGAAAAAATAAGCGGGACAAGTT 1350  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
1351 TGGAGAGATATTACCGGAATAGGACAGCACCGTCACCAATTAATCAGA 1400  
467 pGlyTyrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484  
1401 CGATGGGTAAATTTCTGTTAATGGAGGGTCGGTTTCGGTTGGGTGA 1450  
484 ysgLn 485  
|||||  
1451 AGCAA 1455

seq\_name: gb\_pat:AR143217

seq\_documentation\_block:  
LOCUS AR143217 1455 bp DNA PAT 08-AUG-2001

DEFINITION Sequence 13 from patent US 6204232.

ACCESSION AR143217

VERSION AR143217.1 GI:15104503

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1455)

-AUTHORS Borchert,T.Vedel., Svendsen,A., Andersen,C., Nielsen,B.,

Nissen,T.Lauesgaard and Kj.ae butted.rulff,sslashedren.  
.alpha.-amlase mutants  
Patent: US 6204232-A 13 20-MAR-2001;  
FEATURES  
source Location/Qualifiers  
1..1455  
BASE COUNT 461 a 248 c 361 g 385 t  
ORIGIN

alignment\_scores:

Quality: 2613.00 Length: 485

Ratio: 5.421 Gaps: 0

Percent Similarity: 99.381 Percent Identity: 95.052

alignment\_block:

US-590-375-2 x AR143217 ..

Align seg 1/1 to: AR143217 from: 1 to: 1455

1 HlSHlAsnGlyThrAsnGlyThrMetGlnTyrPheGluTrpHisLe 17  
|||||  
1 CATCATATGGAACAATGGTACTATGATGCAATATTTCTGAATGATATT 50

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34  
|||||

51 GCCAATGACGGGAATCATTTGGACAGGTTGAGGATGACGAGCTAACT 100  
|||||

34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50  
|||||

101 TAAAGATTAAGGGATACAGCTGATGGATGCCACCTGCATGGAGGGG 150  
|||||

51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl 67  
|||||

151 ACTTCCAGATGATGATAGGTTATGGAGCCTATGATTTATATATGATCTGG 200  
|||||

67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
|||||

201 AGAGTTTAAACAGAGGGGACGGTTCGTACAAAATATGGAAACCAACCC 250  
|||||

84 lNLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
|||||

251 AGCTACAGGCTCGGTGACCTCTTTAAAAAATAACGGCATTTCAGGTATAT 300  
|||||

101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||

301 GGTGATGTCGTCAATCAATAAGGTGGAGCAGATGGTACGGAATTTGT 350  
|||||

117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134  
|||||

351 AAATCGGTAGAGAGTGAATCGGAGCAACCGAAACCCAGGAACCTCAGGAG 400  
|||||

134 lutyTrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
|||||

401 AGTATGCATAGACGGTGGACAAAGTTTGATTTCTCGAAGAGGAAT 450  
|||||

151 ThrHisSerAsnPhelLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
|||||

451 AACCAATTCAGCTTTAAAGTGGGCTGGTATCATTTTGTATGGACAGATTG 500  
|||||

167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
|||||

501 GGATAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAAACAG 550  
|||||

184 lYlYsAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
|||||

551 GCAAGCCCTGGGACTGGGAAGTCGATACAGAGAAATGGCAACTATGACTAT 600  
|||||

201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
|||||

601 CTTATGTATCGACGCTGGATATGGATCCACCCAGAAAGTAATACATGAAC 650  
|||||

217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
|||||

|||||  
651 TAGAACTGGGAGCTGGTATACCAATACACTGAACCTTGATGATTTA 700  
234 rgileAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
701 GAATAGATGCGAGTGAACATATAAAATATAGCTTTACGAGAGATGGCTT 750  
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
751 ACACATGCGGTACACACACAGGTAAACCAATGTTTCAGTGGCTGAGTT 800  
267 eTrpLysAsnAspLeuAlaLileGluAsnTyrLeuAsnLysThrSert 284  
801 TTGGAAAAATGACCTTGGTCAATGAAACCTATTGTAATAAAACAAGTT 850  
284 rPasnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
851 GGAATCACTCGGTGTTGATGTTCTCTCCACTATAATTTGTACAATGCA 900  
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
901 TCTAATAGCGGTGTTATGATGATGAGAAATATTTAAATGCTTCTGT 950  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
951 GGTGCAAAAACATCCAACACATGCGGTACTTTTGTGATAAACCATGATT 1000  
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
1001 CTCAGCCCGGGGAAGCATGTTGAATCCCTTTGTCAACAATGTTTAAACCA 1050  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
1051 CTTGCATATGCTTGGTCTGCACAGGAACAAGTTATCTCTCCGTATT 1100  
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMethLys 384  
1101 TTATGGGGATTACTACGGTATCCCAACCCATGGTGTCCGGCTATGAAAT 1150  
384 erLysIleAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
1151 CTAAGTAGACCCCTTCTGTCAGGCACGTCAAACTTTTGCCTATGGTAGC 1200  
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTyrThrArgGluCl 417  
1201 CAGCATGATTACTTTGATCATCATGATATATCGTTGGACAAAGAGGG 1250  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
1251 AAATAGCTCCCATCCAAATTCAGGCCTTGCCACCATTATGTCAGATGGTC 1300  
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyClnVal 450  
1301 CAGGTGGTAACAATAGGATGATGTGGGGAATAATAAGCGGACAAGTT 1350  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
1351 TGGAGATATTACCGGAAATAGGACAGGCACCGCTCACAAATTAATGCAGA 1400  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484  
1401 CGGATGGGGTAATTCCTCTGTTAATGGAGGTCCTCGTTCGGTTTGGGTGA 1450  
484 ysGln 485  
1451 AGCAA 1455

seq\_name: gb\_pat:AR087556

seq\_documentation\_block:

LOCUS AR087556 1458 bp DNA PAT 07-SEP-2000  
DEFINITION Sequence 11 from patent US 5989169.  
ACCESSION AR087556

VERSION AR087556.1 GI:10014319  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1458)  
AUTHORS Svendsen,A., Bisg.ang.rd-Frantzen,H. and Borchert,T.Vedel.  
TITLE .alpha.-amylase mutants  
JOURNAL Patent: US 5989169-A 11 23-NOV-1999;  
FEATURES Location/Qualifiers  
source  
1..1458  
BASE COUNT 463 a 248 c 361 g 386 t  
ORIGIN  
  
alignment\_scores:  
Quality: 2613.00 Length: 485  
Ratio: 5.421 Gaps: 0  
Percent Similarity: 99.381 Percent Identity: 95.052  
  
alignment\_block:  
US-09-590-375-2 x AR087556 ..  
  
Align seg 1/1 to: AR087556 from: 1 to: 1458  
  
1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
|||||  
1 CATATAATGGAACAATGGTACTATGATGCAATATTTCCGAATGGTATTT 50  
  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34  
|||||  
51 GCCAAATGACGGGAATCATTTGGAACAGGTTGAGGGATGACGACGCTAACT 100  
  
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50  
|||||  
101 TAAAGAGTAAAGGGATAACAGCTGTATGGATCCCACTGCATGGAAGGG 150  
  
51 ThrSerGlnAsnAspValGlyGlyAlaTyrAspLeuTyrAspLeuG 67  
|||||  
151 ACTTCCCAAGATGATGAGTTATGGCCCTATGATTTATATGATCTTGG 200  
  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerg 84  
|||||  
201 AGAGTTTAAACCAAGAGGGCGGTTTCGTACAAATATGGAACACGCAACC 250  
  
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
|||||  
251 AGCTACAGGCTGCGGTGACCTCTTTTAAAAAATACGGCATTTCAGGTATAT 300  
  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||  
301 GGTGATGTCGTATGAATCATAAAGGTGGAGCAGATGTTACGGAATTTGT 350  
  
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134  
|||||  
351 AAATCGGTAGAAAGTGAATCGGAGCAACCGAAACCCAGAAACCTCAGGAG 400  
  
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
|||||  
401 AGTATGCAATAGACGCTGGACAAAGTTTGTATTTCTTGGGAAGAGGAAT 450  
  
151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
|||||  
451 AACCATTCAGCTTTAAGTGGCTGGTATCATTTTGTATGGGACAGATTG 500  
  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThr 184  
|||||  
501 GGATCAGTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAG 550  
  
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
|||||  
551 GCAAGGCCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT 600

201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
|||||  
601 CTTATGTATGCACGTGGATGGATGATCCAGAAAGTAATACATGAAT 650  
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
|||||  
651 TAGAACTGGGAGTGTGTAATACGAATACACATGAACCTTGATGGATT 700  
234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
|||||  
701 GAATAGATCGATGAAACATATAAATAATATAGCTTACGAGAGATTGGCTT 750  
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
|||||  
751 ACACATGTGGTAACACACAGGTAACCAATGTTTGCAGTGGCTGAGTT 800  
267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
|||||  
801 TTGGAAAAATGACCTTGGTGCAATGGAACACTATTTGAATAAAACAAGTT 850  
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
|||||  
851 GGAATCACTCGGTGTTGATGTTCTCTCCACTATATAATTTGTACAATGCA 900  
301 SerAsnSerClyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
|||||  
901 TCTAATAGCGGTGGTTATTATGATATAGAAATATTTTAAATGGTTCGT 950  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
|||||  
951 GTGCAAAACATCCAAACACATGCGCTTACTTTTGTGATAACCATGATT 1000  
334 eGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
|||||  
1001 CTCAGCCCGGGAAGCATTTGGAATCCTTTGTTCAACAATGGTTAAACCA 1050  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
|||||  
1051 CTTGCATATGCATGGTCTGACAGGGAAACAGGTTATCCTTCCTGATTT 1100  
367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLys 384  
|||||  
1101 TTATGGGATTACTACGGTATCCCAACCCATGGTGTCCGGCTATGAAAT 1150  
384 eLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
|||||  
1151 CTAAATAGACCCCTCTCTGCAAGGACGTCAAACTTTTCCTATGTGTACG 1200  
401 GlnHisAspTyrPheAspHisAspIleIleGlyTrpThrArgGluG 417  
|||||  
1201 CAGCATGATTACTTTCATCATGATATATTCGGTTGGACAGAGAGGG 1250  
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
|||||  
1251 AAATAGCTCCCATCCAAATTCAGGCTTCCCAACCATTAATGTACAGATGGTC 1300  
434 roGlyClyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
|||||  
1301 CAGGTGGTAACAAATGGATGTATGTGGGAAAAATAAAGCGGACAAAGTT 1350  
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
|||||  
1351 TGGAGAGATATTACCGAAATAGGACAGGACCGCTCACAAATTAATCCAGA 1400  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484  
|||||  
1401 CGGATGGGTAATTTCTCTGTTAATGGAGGGTCCGTTTCGGTTTGGGTGA 1450  
484 ysGln 485  
|||||  
1451 AGCAA 1455

seq\_name: gb\_pat:AR027255  
seq\_documentation\_block: 1455 bp DNA PAT 29-SEP-1999  
LOCUS AR027255 Sequence 5 from patent US 5856164.  
DEFINITION AR027255  
ACCESSION AR027255  
VERSION AR027255.1 GI:5938095  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1455)  
AUTHORS Outtrup,H., Bisq,ang.rd-Frantzen,H., stergaard,P.Rahbek,  
Rasmussen,M.Dolberg and Van Der Zee,P.  
TITLE Alkaline bacillus amylase  
JOURNAL Patent: US 5856164-A 5 05-JAN-1999;  
FEATURES  
source 1. .1455  
location/Qualifiers  
BASE COUNT 473 a 227 c 352 g 403 t  
ORIGIN  
alignment\_scores:  
Quality: 2440.00 Length: 485  
Ratio: 5.148 Gaps: 0  
Percent Similarity: 97.732 Percent Identity: 86.598  
alignment\_block:  
US-09-590-375-2 x AR027255 ..  
Align seg 1/1 to: AR027255 from: 1 to: 1455

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
|||||  
1 CATCATATGGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTT 50  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34  
|||||  
51 GCCTAATGATGGGAATCACTGGAAATAGATTAGAGATGATGCTAGTAATC 100  
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50  
|||||  
101 TAAGAAATAGAGGTATACCGCTATTGGATTCCGCTCGCTGGAAGGG 150  
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67  
|||||  
151 ACTTCGCAAAATGATGGGGTATGGAGCCTATGATCTTTATGATTTAGG 200  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
|||||  
201 GGAATTTAATCAAAAGGGACGGTTCGTACTAAGTATGGGACACGATGTC 250  
84 lInLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
|||||  
251 AATGGAGTCTCCATCCATGCTTTTAAAGAATAATGCGCTTCAAGTTTAT 300  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
|||||  
301 GGGGATGTAGTGTATGAACCATAAAGGAGGAGCTGATGCTACAGAAACGT 350  
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly 134  
|||||  
351 TCTTGTCTGCGAGGTGAATCCAAATTAACCGGAATCAAGAAATATCTGGGG 400  
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150  
|||||  
401 ACTACACAATTGAGGCTTGACTAAGTTTATTTCCAGGAGGGGCTAAT 450  
151 ThrHisSerAsnPhelystTrpArgTrpTyrHisPheAspGlyThrAspTr 167  
|||||  
451 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTTCGATGGTGTAGATTG 500

```
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
501 GGATCAATCAGCAATTCACAAATCCTATCTACAAATTCGAGGTGATG 550
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
184 lYsAlaTAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
551 GTAAGGCATGGGATGGGAAGTAGATTCGGAAATGGAATATATGATTAT 600
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
601 TTAATGTATGCAGATGTAGATATGGATCATCCGGAGGTAGTAATGAGCT 650
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
651 TAGAAGATGGGAGAATGGTATACAAATACAAATAAATCTTCATGGATTTA 700
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
234 rGleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
701 GGATCGATGGGTGAAGCATATTAAATATAGCTTTACACGTGATGGTTG 750
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
751 ACCATGTAGAACGCAACGGGAAGAATGTTCTGCTGTGCTGAATT 800
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSert 284
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
801 TTGGAAAATGATTTAGTGCTGGAGAACTATTAAATAAAACAACACT 850
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
284 rPAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
851 GGAATCATCTGCTTGGATGTCCTCCCTTCATTATATATCTTTAAGCGG 900
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
901 TCAATATGTGAGGCAACTATGACATGCGCAAACTTCTTAATGGAACGGT 950
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
951 TGTTCAAAAGCATCCAAATGATGCGGTAACTTTTGTGATAATCACGATT 1000
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
334 erGlnProGlyGluAlaLeuGlnSerPheValGlnSerTrpPheLysPro 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1001 CTCAACTGGGGAATCAATAGAATCATTTGTACAAAGAATGGTTAAGCCA 1050
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1051 CTTCCTTATGGCTATTATTAACAAGAGACAAGGCTATCCCTCTGCTT 1100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
367 eTyrGlyAspTyrTrpGlyIleProThrHisGlyValProSerMetLys 384
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1101 CTATGGTGACTACTATGGAATTCACACACATAGTGTCCACGAATGAAG 1150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
384 erLysIleAspProLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1151 CCAAGATGATCCCAATCTAGAGCGGTCAAAATTTTGCAATATGGACA 1200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluG 417
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1201 CAACATGATTATTTTGACCATCAATAATATATATCGATGGACACGTGAAG 1250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1251 AAATACCACGCATCCCAATTCAGGACTTGCACATATCATGTCGGATGGC 1300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1301 CAGGGGAGAGAAATGGATGTACAGGGCAAAATAAAGCAGGTCAAGTT 1350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1351 TGGCATCATCACTGGAAATAAACAGGACAGCTTACGATCAATGACAGA 1400
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
467 pGlyTrpGlyAsnPhetrValAsnGlyGlyAlaValSerValTrpValL 484
```

```
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1401 TGGATGGCTAAATTTTCAGTAATGAGGATCTGTTTCCATTTGGGTGA 1450
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
484 ySgln 485
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1451 AACGA 1455
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
seq_name: gb_pat:AR049518
seq_documentation_block:
LOCUS AR049518 1455 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5824531.
ACCESSION AR049518
VERSION AR049518.1 GI:6005557
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Outtrup,H., Bisg,ang.rd-Frantzen,H., stergaard,P.Rahbek,
Rasmussen,M.Dolberg and Van der Zee,P.
TITLE Alkaline bacillus amylase
JOURNAL Patent: US 5824531-A 5 20-OCT-1998;
FEATURES
SOURCE Location/Qualifiers
1.1455
/organism="unknown"
BASE COUNT 473 a 227 c 352 g 403 t
ORIGIN
alignment_scores:
Quality: 2440.00 Length: 485
Ratio: 5.148 Gaps: 0
Percent Similarity: 97.732 Percent Identity: 86.598
alignment_block:
US-09-590-375-2 x AR049518
Align seg 1/1 to: AR049518 from: 1 to: 1455
1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 CATCATATGGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTT 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 GCCTAATGATGGGATCACTCGAATAGATTAAAGATGATGCTAGTAATC 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 TAAGAAATAGAGGTATAACCGCTATTTGGATTCCGCTCGCTGGAAGGG 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 ACTTCGCAAAATGATGGGGTATGGGACCTATGATCTTTATGATTAGG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 GGAATTTAATCAAAAGGGGACGGTTCGTACTAAGTATGGGACACGTAGTC 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 AATTTGGAGTCTGCCATCCATCGCTTTAAGAAATAATGGCGTTCAAGTTAT 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 GGGATGTAGTGATGACCAATAAAGGAGGAGCTGATGCTACAGAAACGT 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 TCTTGCTGTCGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGG 400
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
```

1301 CAGGGCGAGAGAAATGGATGTACGTAGGCGAAATAAAGCAGGTCAAGTT 1350  
451 TtpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
1351 TGGCATGACATACATGGAATAAACCAGGACAGTTACCATCAATCCAGA 1400  
467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484  
1401 TGGATGGGCTAATTTTTCAGTAAATGGAGGATCTGTTTCCATTGGGTGA 1450  
484 ysGln 485  
1451 AACA 1455  
seq\_name: gb\_pat:AR104349  
seq\_documentation\_block: 1455 bp DNA PAT 14-FEB-2001  
LOCUS AR104349  
DEFINITION Sequence 5 from patent US 6093562.  
ACCESSION AR104349  
VERSION AR104349.1 GI:12817057  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1455)  
AUTHORS Bisg.ang.rd-Frantzen,H., Svendsen,A. and Borchert,T.Vedel.  
TITLE Amylase variants  
JOURNAL Patent: US 6093562-A 5 25-JUL-2000;  
FEATURES Location/Qualifiers  
source  
1. .1455  
/organism="unknown"  
BASE COUNT 473 a 227 c 352 g 403 t  
ORIGIN  
alignment\_scores:  
Quality: 2440.00 Length: 485  
Ratio: 5.148 Gaps: 0  
Percent Similarity: 97.732 Percent Identity: 86.598  
alignment\_block:  
US-09-590-375-2 x AR104349 ..  
Align seg 1/1 to: AR104349 from: 1 to: 1455  
1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17  
1 CATCATATGGGACAAATGGGACGATGATGCAATACTTTGAATGGCAGCT 50  
17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34  
51 GCCTAATGATGGGAATCACTGGAATAGATTAAAGATGATGCTAGTAATC 100  
34 euLysSerLysGlyIleThrAlaValTrpIleProAlaTrpLysGly 50  
101 TAAGAAATAGAGGTATAACCGCTATTTGGATTCCGCTCGCTGGAAGGG 150  
51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuG 67  
151 ACTTCGCAAAATGATGGGGATGGGCGTATGAGCTATGATCTTTATGATTAG 200  
67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84  
201 GGAATTTAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGATGTC 250  
84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100  
251 AATTGGAGCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTTAT 300  
101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117  
301 GGGGATGTAGTGTACCATTAAGGAGGAGGCTGATGCTACAGAAAACGT 350

401 ACTACACAATTGAGGCTTGAGCTTAAGTTTCCAGGAGGGGTAAT 450  
151 ThrHisSerAsnPhelYsTrpArgTtpTyrHisPheAspGlyThrAspTr 167  
451 ACATCTCAGACTTAAATGGCGTGGTATCATCTTCATGGTGTAGATTG 500  
167 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184  
501 GGATCAATCAGCACAATTCAAAATCGTATCTACAAATCCGAGGTTGATG 550  
184 lYlYsAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200  
551 GTAAGGCATGGGATGGGAAGTAGATTCGGAATGGAATATGATTAT 600  
201 LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 217  
601 TTAATGTATGAGATGATAGATGATGATGATGATGATGATGATGATG 650  
217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 234  
651 TAGAAGATGGGAGATGCTATACAAATACATTTAAATCTTGATGGATTGA 700  
234 rGileAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 250  
701 GGATCGATCGGTGAAGCATATTAATATAGCTTTACACGTGATTTGGTG 750  
251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267  
751 ACCCATGTAAGAACCACGCGGAAAGAATCTTTGCTGTTGCTGAAT 800  
267 eTrpLysAsnAspLeuAlaIleGluAsnTyrLeuAsnLysThrSerT 284  
801 TTGGAATAATGATTTAGGTGCTTGGAGAACTATTTAAATAAAACAACT 850  
284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300  
851 GGAATCATCTGCTTTGATGATGATGATGATGATGATGATGATGATG 900  
301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317  
901 TCAAAATAGTGGAGCAACTATGACATGGCAAACTTCTTAATGGAACGT 950  
317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAsps 334  
951 TGTTCAAAAGCATCCAAATGATGATGATGATGATGATGATGATGAT 1000  
334 exGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350  
1001 CTCAACTGGGGAATCATTAGAATCATTTGTACAGAATGGTTTAAGCCA 1050  
351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367  
1051 CTTCCTTATGCTTATTTTAAAGAGAACAGGCTATCCCTCTGCTT 1100  
367 eYrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384  
1101 CTATGTGACTACTATGGAATTCACACATAGTGTCCAGCAATGAAAG 1150  
384 exLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400  
1151 CCAGATTCATCCATCTTAGAGGCGCGCAAAATTTTCATATGGAACA 1200  
401 GlnHisAspTyrPheAspHisAspIleIleGlyTrpTrpArgGluG 417  
1201 CAACATGATTTATTTGACCATCATATATAATCCGATGGACACGTGAAG 1250  
417 yaspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
1251 AAATACCGCATCCCAATTCAGGACTTCGACTATCATGTCGGATGGGC 1300  
434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450



117	l	asn	la	val	glu	val	asn	arg	ser	asn	arg	asn	glu	leu	leu	ser	gly	g	134		
1	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
351	t	c	t	t	c	t	c	t	c	t	c	g	a	g	t	t	c	c	400		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
134	l	u	t	y	r	t	h	r	l	e	g	l	a	l	a	t	r	p	h	150	
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
401	a	c	t	a	c	a	a	t	t	g	a	c	c	t	t	g	a	c	450		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
151	t	h	r	h	i	s	e	r	a	s	n	p	h	e	l	y	t	r	p	h	167
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
451	a	c	a	t	a	c	t	c	a	g	a	c	t	t	t	a	a	a	t	500	
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
167	p	a	s	p	g	l	n	s	e	r	a	r	g	l	n	l	e	u	g	184	
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
501	g	a	t	c	a	a	t	c	a	c	a	c	a	a	t	t	c	c	a	550	
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
184	l	y	l	s	a	l	e	r	p	a	s	p	r	p	g	l	u	a	l	200	
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
551	g	t	a	a	g	c	a	t	t	g	g	a	c	t	t	a	a	a	600		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
201	l	e	u	m	e	t	t	y	r	a	a	s	p	i	l	e	a	s	p	h	217
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
601	t	t	a	a	t	g	t	a	t	c	a	g	a	t	g	t	a	g	a	650	
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
217	u	a	r	g	a	s	n	t	r	p	h	r	t	r	p	h	r	t	r	234	
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
651	t	a	g	a	a	g	a	t	t	g	g	a	n	a	t	c	g	t	a	700	
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
234	r	g	i	l	e	a	s	p	a	l	a	v	l	l	y	s	i	l	e	250	
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
701	g	a	t	c	a	t	c	g	c	g	t	a	a	c	a	t	a	t	750		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
251	t	h	r	h	i	s	v	a	r	g	a	s	n	t	r	t	h	r	g	267	
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
751	a	c	c	a	t	g	t	a	g	a	a	c	c	a	r	c	c	g	800		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
267	e	t	r	p	l	y	s	a	s	n	a	s	p	l	e	u	a	l	284		
:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
801	t	t	g	g	a	a	a	a	t	t	a	g	c	t	t	g	g	a	850		
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
284	r	p	a	s	n	h															

417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434  
 1251 AAATACCACGCATCCCAATTCCAGGACTTCGCGACTATCATGTCCGATGGGC 1300  
 434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450  
 1301 CAGGGGAGAGAAATGGATGTACGTAGGGCAAAATAAACGAGTCAAGTT 1350  
 451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467  
 1351 TGGCATGACATAACTGGAAATAAACAGGAAACAGTTCAGATCAATGCAGA 1400  
 467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpVal 484  
 1401 TGGATGGGCTAATTTTTCAGTAATGGAGGATCTGTTCATTTGGGTGA 1450  
 484 ysGln 485  
 1451 AACGA 1455

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2001, 16:58:32 ; Search time 19.44 Seconds  
(without alignments)  
561.425 Million cell updates/sec

Title: US-09-590-375-2

Perfect score: 2713

Sequence: 1 HHNGTNGTMMQYFEWHLPLND.....ADGNGFTVNGCAVSVMVKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2613	96.3	485	2 US-08-446-803-1	Sequence 1, Appli
2	2613	96.3	485	2 US-08-861-837-1	Sequence 1, Appli
3	2613	96.3	485	2 US-08-600-908A-12	Sequence 12, Appl
4	2613	96.3	485	3 US-08-683-838A-12	Sequence 12, Appl
5	2613	96.3	485	3 US-08-600-656-1	Sequence 1, Appli
6	2613	96.3	485	4 US-09-170-670-1	Sequence 1, Appli
7	2613	96.3	485	4 US-09-170-670-7	Sequence 7, Appli
8	2613	96.3	485	4 US-09-193-068-1	Sequence 1, Appli
9	2613	96.3	485	4 US-09-193-068-7	Sequence 7, Appli
10	2613	96.3	485	4 US-09-183-412-1	Sequence 1, Appli
11	2613	96.3	485	4 US-09-183-412-7	Sequence 7, Appli
12	2613	96.3	485	4 US-09-354-191A-1	Sequence 1, Appli
13	2609	96.2	485	4 US-09-264-097-7	Sequence 7, Appli
14	2440	89.9	485	2 US-08-446-803-2	Sequence 2, Appli
15	2440	89.9	485	2 US-08-861-837-2	Sequence 2, Appli
16	2440	89.9	485	3 US-08-600-656-2	Sequence 2, Appli
17	2440	89.9	485	4 US-09-170-670-2	Sequence 2, Appli
18	2440	89.9	485	4 US-09-170-670-8	Sequence 8, Appli
19	2440	89.9	485	4 US-09-193-068-2	Sequence 2, Appli
20	2440	89.9	485	4 US-09-193-068-8	Sequence 8, Appli
21	2440	89.9	485	4 US-09-183-412-2	Sequence 2, Appli
22	2440	89.9	485	4 US-09-183-412-8	Sequence 8, Appli
23	2440	89.9	485	4 US-09-264-097-5	Sequence 5, Appli
24	2440	89.9	485	4 US-09-354-191A-2	Sequence 2, Appli
25	2410	88.8	485	3 US-08-600-656-7	Sequence 7, Appli
26	2410	88.8	485	4 US-09-170-670-6	Sequence 6, Appli
27	2410	88.8	485	4 US-09-193-068-6	Sequence 6, Appli

28 2410 88.8 485 4 US-09-183-412-6 Sequence 6, Appli  
29 2410 88.8 485 4 US-09-354-191A-7 Sequence 7, Appli  
30 1983 73.1 400 4 US-09-264-097-6 Sequence 6, Appli  
31 1910.5 70.4 514 4 US-09-182-859-6 Sequence 6, Appli  
32 1910.5 70.4 514 4 US-09-264-097-8 Sequence 8, Appli  
33 1910.5 70.4 549 1 US-08-720-899-6 Sequence 6, Appli  
34 1910.5 70.4 549 1 US-08-459-610-6 Sequence 6, Appli  
35 1910.5 70.4 549 2 US-08-343-804-6 Sequence 6, Appli  
36 1910.5 70.4 549 2 US-08-687-399-6 Sequence 6, Appli  
37 1910.5 70.4 549 2 US-08-600-908A-6 Sequence 6, Appli  
38 1910.5 70.4 549 3 US-08-683-838A-6 Sequence 6, Appli  
39 1909 70.4 483 1 US-08-468-700-34 Sequence 34, Appl  
40 1909 70.4 483 2 US-08-468-220-32 Sequence 32, Appl  
41 1909 70.4 483 2 US-08-468-698-32 Sequence 32, Appl  
42 1909 70.4 483 2 US-08-704-706A-34 Sequence 34, Appl  
43 1909 70.4 483 3 US-08-890-283-3 Sequence 3, Appli  
44 1909 70.4 483 3 US-08-914-679A-3 Sequence 3, Appli  
45 1909 70.4 483 4 US-09-182-859-2 Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-08-446-803-1  
; Sequence 1, Application US/08446803  
; Patent No. 5824531  
; GENERAL INFORMATION:  
; APPLICANT: Otrup, Helle  
; APPLICANT: Bisgaard-Frantzen, Henrik  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Rasmussen, Michael Dolberg  
; APPLICANT: Van Der Zee, Pia  
; TITLE OF INVENTION: Alkaline Bacillus Amylase  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5824531o No. 5824531disk of No. 5824531th America.  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,803  
; FILING DATE: 01-June-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: 38,711  
; REFERENCE/DOCKET NUMBER: 4157.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 867-0123  
; TELEFAX: (212) 878-9655  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-446-803-1

Query Match 96.3%; Score 2613; DB 2; Length 485;

Best Local Similarity 95.1%; Pred. No. 2.7e-223;  
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPLNDGNNHNRLLRDAANLKRSGITAVWIPPAWKGTQNDVGYGA 60



```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-600-908A-12

Query Match          96.3%; Score 2613; DB 2; Length 485;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGEFNGKQKTVRTKYGTRNQLQAAVTSKNNGIQVYGVVMMHKGADGTEIVNAV 120
Db 61 YDLYDLGEFNGKQKTVRTKYGTRNQLQAAVTSKNNGIQVYGVVMMHKGADGTEIVNAV 120
QY 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
Db 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
QY 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNMGVWYTNLTLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNMGVWYTNLTLDGFRIDAVKH 240
QY 241 IKYSYTRDLWTHVRNTTGRKPMFAVEFWKNDLAAIENYLNKTSWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSYTRDLWTHVRNTTGRKPMFAVEFWKNDLAAIENYLNKTSWNHVSFVDPVPLHYNLYNA 300
QY 301 SNSSGYDFMRNINLNGSVVQKHPHATVFDNDHDSQPCEALESFVQSWFKPLAYALILTRE 360
Db 301 SNSSGYDFMRNINLNGSVVQKHPHATVFDNDHDSQPCEALESFVQSWFKPLAYALILTRE 360
QY 361 QGYPSVFGYDYGIPTHGVPSMKSKIDPLQARQTYAYGTQHDYFQHHDIIGWTREGDSS 420
Db 361 QGYPSVFGYDYGIPTHGVPSMKSKIDPLQARQTYAYGTQHDYFQHHDIIGWTREGDSS 420
QY 421 HPNSGLATIMSDGPGGNKMYGKHKAGQVWRDITGNRSCTVTINADGWNFTVNGGVS 480
Db 421 HPNSGLATIMSDGPGGNKMYGKHKAGQVWRDITGNRSCTVTINADGWNFTVNGGVS 480
QY 481 VVYKQ 485
Db 481 VVYKQ 485

; ADDRESS: No. 60227240 No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-683-838A-12

Query Match          96.3%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60
QY 61 YDLYDLGEFNGKQKTVRTKYGTRNQLQAAVTSKNNGIQVYGVVMMHKGADGTEIVNAV 120
Db 61 YDLYDLGEFNGKQKTVRTKYGTRNQLQAAVTSKNNGIQVYGVVMMHKGADGTEIVNAV 120
QY 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
Db 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKRWYHFDGTDWDSQRLQNKIYKF 180
QY 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNMGVWYTNLTLDGFRIDAVKH 240
Db 181 RGTGKAWDEVDIENGNDYLYMADIDMDHPEVINELRNMGVWYTNLTLDGFRIDAVKH 240
QY 241 IKYSYTRDLWTHVRNTTGRKPMFAVEFWKNDLAAIENYLNKTSWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSYTRDLWTHVRNTTGRKPMFAVEFWKNDLAAIENYLNKTSWNHVSFVDPVPLHYNLYNA 300
QY 301 SNSSGYDFMRNINLNGSVVQKHPHATVFDNDHDSQPCEALESFVQSWFKPLAYALILTRE 360
Db 301 SNSSGYDFMRNINLNGSVVQKHPHATVFDNDHDSQPCEALESFVQSWFKPLAYALILTRE 360
QY 361 QGYPSVFGYDYGIPTHGVPSMKSKIDPLQARQTYAYGTQHDYFQHHDIIGWTREGDSS 420
Db 361 QGYPSVFGYDYGIPTHGVPSMKSKIDPLQARQTYAYGTQHDYFQHHDIIGWTREGDSS 420
QY 421 HPNSGLATIMSDGPGGNKMYGKHKAGQVWRDITGNRSCTVTINADGWNFTVNGGVS 480
Db 421 HPNSGLATIMSDGPGGNKMYGKHKAGQVWRDITGNRSCTVTINADGWNFTVNGGVS 480
QY 481 VVYKQ 485
Db 481 VVYKQ 485

RESULT 4
US-08-683-838A-12
; Sequence 12, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:

```

RESULT 5  
 US-08-600-656-1  
 : Sequence 1, Application US/08600656  
 : Patent No. 6093562  
 : GENERAL INFORMATION:  
 : APPLICANT: Bisgard-Frantzen, Henrik  
 : APPLICANT: Svendsen, Allan  
 : APPLICANT: Borcherdt, Torben Vedel  
 : TITLE OF INVENTION: AMYLASE VARIANTS  
 : NUMBER OF SEQUENCES: 32  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.  
 : STREET: 405 Lexington Avenue, Suite 6400  
 : CITY: New York  
 : STATE: New York  
 : COUNTRY: U.S.A.  
 : ZIP: 10174-6401  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
 : CURRENT APPLICATION DATA: US/08/600.656  
 : APPLICATION NUMBER: US/08/600.656  
 : FILING DATE: 13-FEB-1996  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Lambiris, Elias J.  
 : REGISTRATION NUMBER: 33,728  
 : REFERENCE/DOCKET NUMBER: 4318.204-US  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 212 867 0123  
 : TELEFAX: 212 867 0298  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 485 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: peptide  
 US-08-600-656-1

Query Match 96.3%; Score 2613; DB 3; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 2.7e-223;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 HNGTNGTMMQYFEWHLPLNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGGA 60  
 DB 1 HNGTNGTMMQYFEWHLPLNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGGA 60  
 QY 61 YDLVDLGEFNKGKGVTRTKYGRSLOGAVTSLKNGIQVYGVVNNHKGADGTEMVNAV 120  
 DB 61 YDLVDLGEFNKGKGVTRTKYGRSLOGAVTSLKNGIQVYGVVNNHKGADGTEMVNAV 120  
 QY 121 EVNRSNRNOEISGEYTTIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSRQLQNKIYKF 180  
 DB 121 EVNRSNRNOEISGEYTTIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSRQLQNKIYKF 180  
 QY 181 RGTCKANDWEVDIENGNYDILMYADIMDHPEVINELRNWGVWYTNLNLGDFRIDAVKH 240  
 DB 181 RGTCKANDWEVDIENGNYDILMYADIMDHPEVINELRNWGVWYTNLNLGDFRIDAVKH 240  
 QY 241 IKYSYTRDLWTHVRNTTGKPMFAEAEWKNDLAAIENYLNKTSNNHVSFVDFVPLHYNLYNA 300  
 DB 241 IKYSYTRDLWTHVRNTTGKPMFAEAEWKNDLAAIENYLNKTSNNHVSFVDFVPLHYNLYNA 300  
 QY 301 SNSGGYFDMRNILGNSVQKHPHIAVTFVDNHDSDQPEALESFVQWFKPLAYALILTRE 360  
 DB 301 SNSGGYFDMRNILGNSVQKHPHIAVTFVDNHDSDQPEALESFVQWFKPLAYALILTRE 360

QY 361 QGYPSVFYGDYIGIPTHGVPMSKSKIDPLLOARQTYAYGTQHDYFDHHDIIIGWTRGDS 420  
 DB 361 QGYPSVFYGDYIGIPTHGVPMSKSKIDPLLOARQTYAYGTQHDYFDHHDIIIGWTRGDS 420  
 QY 421 HPNSGLATIMSDGPGGNKWMYVGHKAGQVWRDITGNRSQVTTNADGWGNTVNGGAVS 480  
 DB 421 HPNSGLATIMSDGPGGNKWMYVGHKAGQVWRDITGNRSQVTTNADGWGNTVNGGAVS 480  
 QY 481 VWVKQ 485  
 DB 481 VWVKQ 485  
 RESULT 6  
 US-09-170-670-1  
 : Sequence 1, Application US/09170670  
 : Patent No. 6187576  
 : GENERAL INFORMATION:  
 : APPLICANT: Svendsen, Allan  
 : APPLICANT: Borcherdt, Torben  
 : APPLICANT: Bisgard-Frantzen Henrik  
 : TITLE OF INVENTION: Alpha-Amylase Mutants  
 : FILE REFERENCE: 5276.200-US  
 : CURRENT APPLICATION NUMBER: US/09/170.670  
 : CURRENT FILING DATE: 1998-10-13  
 : EARLIER APPLICATION NUMBER: 1172/97  
 : EARLIER FILING DATE: 1997-10-13  
 : EARLIER APPLICATION NUMBER: 60/063.306  
 : EARLIER FILING DATE: 1997-10-28  
 : NUMBER OF SEQ ID NOS: 22  
 : SOFTWARE: FastSEQ for Windows Version 3.0  
 : SEQ ID NO 1  
 : LENGTH: 485  
 : TYPE: PRT  
 : ORGANISM: Bacillus sp.  
 US-09-170-670-1

Query Match 96.3%; Score 2613; DB 4; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 2.7e-223;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 HNGTNGTMMQYFEWHLPLNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGGA 60  
 DB 1 HNGTNGTMMQYFEWHLPLNDGNHNRRLRDDAANKSKGITAVWIPPAWKGTSONDVGGA 60  
 QY 61 YDLVDLGEFNKGKGVTRTKYGRSLOGAVTSLKNGIQVYGVVNNHKGADGTEMVNAV 120  
 DB 61 YDLVDLGEFNKGKGVTRTKYGRSLOGAVTSLKNGIQVYGVVNNHKGADGTEMVNAV 120  
 QY 121 EVNRSNRNOEISGEYTTIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSRQLQNKIYKF 180  
 DB 121 EVNRSNRNOEISGEYTTIEAWTKFDPGGRNTHSNFKRWYHFDGTDWDSRQLQNKIYKF 180  
 QY 181 RGTCKANDWEVDIENGNYDILMYADIMDHPEVINELRNWGVWYTNLNLGDFRIDAVKH 240  
 DB 181 RGTCKANDWEVDIENGNYDILMYADIMDHPEVINELRNWGVWYTNLNLGDFRIDAVKH 240  
 QY 241 IKYSYTRDLWTHVRNTTGKPMFAEAEWKNDLAAIENYLNKTSNNHVSFVDFVPLHYNLYNA 300  
 DB 241 IKYSYTRDLWTHVRNTTGKPMFAEAEWKNDLAAIENYLNKTSNNHVSFVDFVPLHYNLYNA 300  
 QY 301 SNSGGYFDMRNILGNSVQKHPHIAVTFVDNHDSDQPEALESFVQWFKPLAYALILTRE 360  
 DB 301 SNSGGYFDMRNILGNSVQKHPHIAVTFVDNHDSDQPEALESFVQWFKPLAYALILTRE 360  
 QY 361 QGYPSVFYGDYIGIPTHGVPMSKSKIDPLLOARQTYAYGTQHDYFDHHDIIIGWTRGDS 420  
 DB 361 QGYPSVFYGDYIGIPTHGVPMSKSKIDPLLOARQTYAYGTQHDYFDHHDIIIGWTRGDS 420  
 QY 421 HPNSGLATIMSDGPGGNKWMYVGHKAGQVWRDITGNRSQVTTNADGWGNTVNGGAVS 480  
 DB 421 HPNSGLATIMSDGPGGNKWMYVGHKAGQVWRDITGNRSQVTTNADGWGNTVNGGAVS 480

QY 481 VVVKQ 485  
 Db 481 VVVKQ 485

RESULT 7

US-09-170-670-7  
 ; Sequence 7, Application US/09170670  
 ; Patent No. 6167576  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Bisgaard-Frantzen, Henrik  
 ; TITLE OF INVENTION: Alpha-Amylase Mutants  
 ; FILE REFERENCE: 5276.200-US  
 ; CURRENT APPLICATION NUMBER: US/09/170,670  
 ; CURRENT FILING DATE: 1998-10-13  
 ; EARLIER APPLICATION NUMBER: 1172/97  
 ; EARLIER FILING DATE: 1997-10-13  
 ; EARLIER APPLICATION NUMBER: 60/063,306  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 485  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus sp.  
 US-09-170-670-7

Query Match 96.3%; Score 2613; DB 4; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 2.7e-223;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60  
 Db 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60  
 QY 61 YLDYDLGEFNGKGTVRTKYGTSQLOQAVTSLKNGGIQVYGVVNMHKGADGTEVNAV 120  
 Db 61 YLDYDLGEFNGKGTVRTKYGTSQLOQAVTSLKNGGIQVYGVVNMHKGADGTEVNAV 120  
 QY 121 EVNRSNRNQEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWQSRQLQNKIYKF 180  
 Db 121 EVNRSNRNQEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWQSRQLQNKIYKF 180  
 QY 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240  
 Db 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240  
 QY 241 IKYSYTRDMLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
 Db 241 IKYSYTRDMLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
 QY 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360  
 Db 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360  
 QY 361 QGYPSVFYGDYGIPTGHPVPMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTREGDSS 420  
 Db 361 QGYPSVFYGDYGIPTGHPVPMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTREGDSS 420  
 QY 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGNFTVNGGVS 480  
 Db 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGNFTVNGGVS 480

QY 481 VVVKQ 485  
 Db 481 VVVKQ 485

RESULT 8

US-09-193-068-1  
 ; Sequence 1, Application US/09193068  
 ; Patent No. 6197565  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Kjrulff, S ren  
 ; APPLICANT: Bisgaard-Frantzen, Henrik  
 ; APPLICANT: Andersen, Carsten  
 ; TITLE OF INVENTION: -Amylase Variants  
 ; FILE REFERENCE: 5709.000-US  
 ; CURRENT APPLICATION NUMBER: US/09/193,068  
 ; CURRENT FILING DATE: 1998-11-16  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 485  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus sp.  
 US-09-193-068-1

Query Match 96.3%; Score 2613; DB 4; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 2.7e-223;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60  
 Db 1 HNGTNGTMMQYFEWHLPLNDGNHNRLRDAANLKSKITAVWIPPAWKGTSONDVGYGA 60  
 QY 61 YLDYDLGEFNGKGTVRTKYGTSQLOQAVTSLKNGGIQVYGVVNMHKGADGTEVNAV 120  
 Db 61 YLDYDLGEFNGKGTVRTKYGTSQLOQAVTSLKNGGIQVYGVVNMHKGADGTEVNAV 120  
 QY 121 EVNRSNRNQEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWQSRQLQNKIYKF 180  
 Db 121 EVNRSNRNQEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTDWQSRQLQNKIYKF 180  
 QY 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240  
 Db 181 RGTGKAWDEVDIENGNYDLYADIDMDHPEVINELRNWGVWYTNLNDGFRIDAVKH 240  
 QY 241 IKYSYTRDMLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
 Db 241 IKYSYTRDMLTHVRNTTGKPMFAVEFKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
 QY 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360  
 Db 301 SNSGGYDMRNILNGSVQKHPHATVTFVDNHDSPQGEALSFVQSWFKPLAYALVLTRE 360  
 QY 361 QGYPSVFYGDYGIPTGHPVPMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTREGDSS 420  
 Db 361 QGYPSVFYGDYGIPTGHPVPMKSKIDPLQARQTYAGTQHDYFDHHDIIIGWTREGDSS 420  
 QY 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGNFTVNGGVS 480  
 Db 421 HPNSGLATIMSDGPGGNKMWYVCKHKGAGQVWRDITNRSCTVTINADGNGNFTVNGGVS 480

QY 481 VVVKQ 485  
 Db 481 VVVKQ 485

RESULT 9

US-09-193-068-7  
 ; Sequence 7, Application US/09193068  
 ; Patent No. 6197565  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Kjrulff, S ren  
 ; APPLICANT: Bisgaard-Frantzen, Henrik  
 ; APPLICANT: Andersen, Carsten  
 ; TITLE OF INVENTION: -Amylase Variants  
 ; FILE REFERENCE: 5709.000-US





; EARLIER APPLICATION NUMBER: PA 1998 00936  
; EARLIER FILING DATE: 1998-07-14  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 485  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-183-412-7

Query Match 96.3%; Score 2613; DB 4; Length 485;  
Best Local Similarity 95.1%; Pred. No. 2.7e-223;  
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;  
QY 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60  
Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60  
QY 61 YDLYDLGEFNGKQTVRTKYGTSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120  
Db 61 YDLYDLGEFNGKQTVRTKYGTSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120  
QY 121 EVNRSNRNQETSGEYTIKFTDFPCRGNTHSNFKRWYHFDGTDQSRQLQNKIYKF 180  
Db 121 EVNRSNRNQETSGEYTIKFTDFPCRGNTHSNFKRWYHFDGTDQSRQLQNKIYKF 180  
QY 181 RGTGKAWDEVDTENGNYDLYMTADMDHPEVINELRNNGVWYVNTLNLDGFRIDAVKH 240  
Db 181 RGTGKAWDEVDTENGNYDLYMTADMDHPEVINELRNNGVWYVNTLNLDGFRIDAVKH 240  
QY 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
Db 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
QY 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPGEALSFVQWFKPLAYALVLTRE 360  
Db 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPGEALSFVQWFKPLAYALVLTRE 360  
QY 361 QGYPSVFYGDYIGIPTHGVPSMKSIDPLQARQTYAYGTQHDYFDHDDIIGWTREGDSS 420  
Db 361 QGYPSVFYGDYIGIPTHGVPSMKSIDPLQARQTYAYGTQHDYFDHDDIIGWTREGDSS 420  
QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480  
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480  
QY 481 VVVKQ 485  
Db 481 VVVKQ 485

RESULT 12  
US-09-354-191A-1  
; Sequence 1, Application US/09354191A  
; Patent No. 6297038  
; GENERAL INFORMATION:  
; APPLICANT: Bisgaard-Frantzen, Henrik  
; APPLICANT: Svendsen, Allan  
; APPLICANT: Borchert, Torben Vedel  
; TITLE OF INVENTION: AMYLASE VARIANTS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.  
; STREET: 405 Lexington Avenue, Suite 6400  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10174-6401  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/354,191A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/600,656  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lambiris, Elias J.  
; REGISTRATION NUMBER: 33,728  
; REFERENCE/DOCKET NUMBER: 4318.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 867 0123  
; TELEFAX: 212 867 0298  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-354-191A-1  
Query Match 96.3%; Score 2613; DB 4; Length 485;  
Best Local Similarity 95.1%; Pred. No. 2.7e-223;  
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;  
QY 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60  
Db 1 HHNGTGTMMQYFEWHLPLNDGNHNRLRDDAANKSGITAVWIPPAWKGTSONDVGYGA 60  
QY 61 YDLYDLGEFNGKQTVRTKYGTSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120  
Db 61 YDLYDLGEFNGKQTVRTKYGTSLQLOGAVTSLKNGGIQVYGVVNMHKGADGTEMYNAV 120  
QY 121 EVNRSNRNQETSGEYTIKFTDFPCRGNTHSNFKRWYHFDGTDQSRQLQNKIYKF 180  
Db 121 EVNRSNRNQETSGEYTIKFTDFPCRGNTHSNFKRWYHFDGTDQSRQLQNKIYKF 180  
QY 181 RGTGKAWDEVDTENGNYDLYMTADMDHPEVINELRNNGVWYVNTLNLDGFRIDAVKH 240  
Db 181 RGTGKAWDEVDTENGNYDLYMTADMDHPEVINELRNNGVWYVNTLNLDGFRIDAVKH 240  
QY 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
Db 241 IKYSYTRDMLTHVRNTTGGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVDFVPLHYNLYNA 300  
QY 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPGEALSFVQWFKPLAYALVLTRE 360  
Db 301 SNSSGGYDMRNILNGSVVQKHPHATVFDVNDHDSQPGEALSFVQWFKPLAYALVLTRE 360  
QY 361 QGYPSVFYGDYIGIPTHGVPSMKSIDPLQARQTYAYGTQHDYFDHDDIIGWTREGDSS 420  
Db 361 QGYPSVFYGDYIGIPTHGVPSMKSIDPLQARQTYAYGTQHDYFDHDDIIGWTREGDSS 420  
QY 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480  
Db 421 HPNSGLATIMSDGPGGNKMWYVGNKAGQVWRDITGNRTGTGTINADGWNFTVNGGVS 480  
QY 481 VVVKQ 485  
Db 481 VVVKQ 485  
RESULT 13  
US-09-264-097-7  
; Sequence 7, Application US/09264097  
; Patent No. 6287826  
; GENERAL INFORMATION:  
; APPLICANT: No. 6287826man, Barrie Edmund  
; APPLICANT: Hendriksen, Hanne Vang

```

RESULT 14
US-08-446-803-2
; Sequence 2, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
; APPLICANT: Ottrup, Helle
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Ostergaard, Peter, Rahbek
; APPLICANT: Rasmussen, Michael Dolberg
; APPLICANT: Van Der Zee, Pia
; TITLE OF INVENTION: Alkaline Amylase
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5824531o No. 5824531disk of No. 5824531th America

```

US-08-861-837-2  
; Sequence 2, Application US/08861837  
; Patent No. 5856164  
; GENERAL INFORMATION:  
; APPLICANT: Otttrup, Helle  
; APPLICANT: Bisgard-Frantzen, Henrik  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Rasmussen, Michael Dolberg  
; APPLICANT: Van Der Zee, Pia  
; TITLE OF INVENTION: Alkaline Bacillus Amylase  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5856164 No. 5856164disk of No. 5856164th America  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,837  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,803  
; FILING DATE: 01-June-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: 38,711  
; REFERENCE/DOCKET NUMBER: 4157.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 867-0123  
; TELEFAX: (212) 878-9655  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-861-837-2

Query Match 89.9%; Score 2440; DB 2; Length 485;  
Best Local Similarity 86.6%; Pred. No. 5.6e-208;  
Matches 420; Conservative 40; Mismatches 25; Indels 0; Gaps 0;

QY	1	HHNGTNGTMMQYFEWHLPPNDGNHWNRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA	60
DB	1	HHNGTNGTMMQYFEWHLPPNDGNHWNRLRDDAANLKSIGITAVWIPPAWKGTSONDVGYGA	60
QY	61	YDLYDLGEFNGKGTVRTKYGTSQLQGAVALSKNNGIQVYGDVVMNHKGGADGTEMVNAV	120
DB	61	YDLYDLGEFNGKGTVRTKYGTSQLQGAVALSKNNGIQVYGDVVMNHKGGADGTEMVNAV	120
QY	121	EVNRNRNQEISGEYTIETATKFDGPGRGNTSHNFKRWYHFDGTDWDSRQLQNKIYKF	180
DB	121	EVAPNPNRQEISGDYTIETATKFDGPGRGNTSDFKRWYHFDGVDWDSRQFQNRIFYK	180
QY	181	RGTKANDWEVDYENGNYDLYMADIDMDHPEVINELRNNGVWYTNLTNLDGFRIDAVKH	240
DB	181	RGDGKANDWEVDSENGNYDLYMADVDMDHPEVINELRNNGEWYTNLTNLDGFRIDAVKH	240
QY	241	IKYSYTRDLWLTHTVANTTKPKMFAVAEFKNDLAAIENLNKTSNNHVSFVDFPLHNLNA	300
DB	241	IKYSFTRDWLTHTVRNATGKEMFAVAEFKNDLGALENYLNKTNWNHVSFVDFPLHNLNA	300
QY	301	SNSGGYFDMRNILNGSVVQKHPHVAFTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE	360

Db	301	SNSGGYDMAKLLNGTVVQKHPHVAFTFVDNHDSPQGESLESFVQEWFKPLAYALILTRE	360
QY	361	QGYPSVFYGDYVGIPTHTGVPMSKSIDPLLAQARTYAVGTQHDYFDHDDIIGWTREGDSS	420
Db	361	QGYPSVFYGDYVGIPTHTGVPMSKSIDPLLAQARTYAVGTQHDYFDHDDIIGWTREGDSS	420
QY	421	HPNSGLATIMSDGPGGNKMYVGVKHKAGQVWRDITGNRSQGTVTINADGWNFTVNGGAVS	480
Db	421	HPNSGLATIMSDGPGGKMYVGVQNKAGQVWHDTITGNKPGTVTINADGWNFVNGGAVS	480
QY	481	VWVKQ	485
Db	481	IWKVR	485

Search completed: November 28, 2001, 16:58:33  
Job time: 206 sec

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: November 28, 2001, 16:58:04 ; Search time 33.83 Seconds  
(without alignments)  
1061.943 Million cell updates/sec

Title: US-09-590-375-2

Perfect score: 2713

Sequence: 1 HHNGTNGTMQYFEWHLFND.....ADGNGFTNGGAVSVVVKQ 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

A\_Geneseq\_1101.\*  
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2713	100.0	516	18 AAW11326	Alkaline liquefyin
2	2704	99.7	485	19 AAW79904	Liquefied alkaline
3	2700	99.5	516	21 AAB35714	Mutant alpha-amylase
4	2613	96.3	485	18 AAW31499	Bacillus sp. alpha
5	2613	96.3	485	19 AAW48260	Bacillus sp. alpha
6	2613	96.3	485	20 AAY25150	Bacillus sp. alpha
7	2613	96.3	485	20 AAY15415	Bacillus strain NC
8	2613	96.3	485	20 AAY15421	Teramyl-like alph
9	2613	96.3	485	20 AAY07381	Wild type Teramyl
10	2613	96.3	485	20 AAY07391	Wild type Teramyl
11	2613	96.3	485	21 AAY99602	Bacillus parent Te

12	2613	96.3	485	21	AA999608	Bacillus Teramyl-
13	2611	96.2	485	17	AAW12113	Alpha-amylase vari
14	2610	96.2	485	17	AAW12129	Alpha-amylase vari
15	2610	96.2	485	17	AAW12130	Alpha-amylase vari
16	2610	96.2	485	17	AAW12119	Alpha-amylase vari
17	2610	96.2	485	17	AAW12120	Alpha-amylase vari
18	2610	96.2	485	17	AAW12121	Alpha-amylase vari
19	2610	96.2	485	17	AAW12118	Alpha-amylase vari
20	2610	96.2	485	17	AAW12102	Alpha-amylase vari
21	2610	96.2	485	17	AAW12103	Alpha-amylase vari
22	2610	96.2	485	17	AAW12104	Alpha-amylase vari
23	2610	96.2	485	17	AAW12105	Alpha-amylase vari
24	2610	96.2	485	17	AAW12106	Alpha-amylase vari
25	2610	96.2	485	17	AAW12107	Alpha-amylase vari
26	2610	96.2	485	17	AAW12108	Alpha-amylase vari
27	2610	96.2	485	17	AAW12098	Alpha-amylase vari
28	2610	96.2	485	17	AAW12099	Alpha-amylase vari
29	2610	96.2	485	17	AAW12100	Alpha-amylase vari
30	2609	96.2	485	17	AAW12114	Alpha-amylase vari
31	2609	96.2	485	17	AAW12117	Alpha-amylase vari
32	2608	96.1	485	17	AAW12127	Alpha-amylase vari
33	2608	96.1	485	17	AAW12128	Alpha-amylase vari
34	2608	96.1	485	17	AAW12131	Alpha-amylase vari
35	2608	96.1	485	17	AAW12122	Alpha-amylase vari
36	2608	96.1	485	17	AAW12123	Alpha-amylase vari
37	2608	96.1	485	17	AAW12124	Alpha-amylase vari
38	2608	96.1	485	17	AAW12125	Alpha-amylase vari
39	2608	96.1	485	17	AAW12126	Alpha-amylase vari
40	2607	96.1	485	17	AAW12111	Alpha-amylase vari
41	2607	96.1	485	17	AAW12112	Alpha-amylase vari
42	2607	96.1	485	17	AAW12101	Alpha-amylase vari
43	2606	96.1	485	17	AAW12144	Alpha-amylase vari
44	2606	96.1	485	17	AAW12110	Alpha-amylase vari
45	2605	96.0	485	17	AAW12109	Alpha-amylase vari

## ALIGNMENTS

RESULT 1  
AAW11326  
ID AAW11326 standard; Protein; 516 AA.  
XX  
AC AAW11326;  
XX  
XX 11-NOV-1997 (first entry)  
DT  
XX  
DE Alkaline liquefying alpha-amylase.  
XX  
KW Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent;  
KW starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance;  
KW alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;  
KW dish-washing detergent; starch.  
XX  
XX Bacillus species KSM-API378.  
OS  
PN WO9700324-A1.  
XX  
PD 03-JAN-1997.  
XX  
PF 14-JUN-1996; 96WO-JP01641.  
XX  
XX 14-JUN-1995; 95JP-0147257.  
PR  
XX (KAOS ) KAO CORP.  
PA  
XX  
XX Ara K, Hatada Y, Ito S, Kawai S, Ozaki K.  
PI  
XX WPI: 1997-118708/11.  
DR  
XX N-PSDB; AAT51339.  
DR  
XX DNA encoding alkaline liquefying alpha-amylase - useful in  
PT dish-washing and laundry detergents for removal of starch dirt  
PT

Claim 2; Page 23-26; 40pp; English.  
 This sequence represents an alkaline liquefying alpha-amylase.  
 Alpha-amylase is an enzyme that acts on starch-related polysaccharides,  
 hydrolysing the alpha-1,4-glucoside bond of the polysaccharide molecule.  
 Alkaline liquefying alpha-amylases exhibit resistance to surfactants used  
 in detergents, and decompose starch or starch-related polysaccharides in  
 a highly random manner. The bacillus species KSM-AP1378, from which this  
 sequence was isolated, is an alkalophilic Bacillus strain. It was  
 isolated from soil in the vicinity of the city of Tochigi. The enzyme is  
 useful in improving the efficiency of dish-washing and laundry  
 detergents, particularly on starch dirt.  
 Sequence 516 AA;  
 SQ

	Key	Location/Qualifiers	
FH	Misc-difference	202	
FT	/note=	"can be deleted or substituted by another amino acid residue such as Thr, Ile, Leu, Ala, Val Or Ser"	
FT			
FT			
XX	W09844126-A1.		
XX	08-OCT-1998.		
XX	31-MAR-1998;	98WO-JP01464.	
XX	31-MAR-1997;	97JP-0080299.	
PA	(KAOS ) KAO CORP.		
PI	Hatada Y, Ikawa K, Ito S;		
XX	WPT; 1998-542707/46.		
DR	Bacillus derived alpha amylase having mutation at position 202 -		
PT	has optimum pH in alkaline conditions and high tolerance to		
PT	oxidants, useful for production of detergent compositions		
XX	Claim 1; Page 19-21; 42pp; Japanese.		
PS	The present sequence represents Bacillus licheniformis liquefied alkaline		
XX	alpha-amylase. The present invention describes mutated forms of the		
CC	liquefied alkaline alpha-amylase derived from Bacillus species KSM-AP1378		
CC	(FERM BP-3048), having the methionine residue at position 202 either		
CC	deleted or substituted by another amino acid, such as threonine,		
CC	isoleucine, leucine, alanine, valine or serine. The mutated enzyme may		
CC	have other mutations (such as deletion of arginine or glycine at		
CC	positions 181 and 182, respectively) but at least 95.2% homologous to		
CC	the original enzyme. The mutated enzyme has optimum pH in alkaline		
CC	conditions, a high alpha amylase activity, and a high and sustained		
CC	tolerance to oxidising substances. The enzyme may be used in the		
CC	formulation of liquid, powder or granular detergent compositions,		
CC	especially those containing bleaches and oxidants. The enzyme retains		
CC	high activity in the presence of bleaches and oxidants allowing improved		
CC	detergent formulations to be produced.		
XX			
SQ	Sequence	485 AA;	
	Query Match	99.7%; Score 2704; DB 19; Length 485;	
	Best Local Similarity	99.8%; Pred. No. 2.2e-218;	
	Matches	484; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
Qy	1 HNGTGTMMQYFEWHLPDNGHNHRLRDDAANLKSKGITAWIIPAWKGTQNDDVGYGA	60	
Db	1 hngtnglmmgtfewhlpnqdnghwnrlrddaanlksgitavippawkgtsqndvgvga	60	
Qy	61 YDLGLGEBFNQKGVTRTKYGRSQLGQAVTSLKNNGIOVGDVWNHKGAGDTGMNNAV	120	
Db	61 ydlydlgefndkgtvrtkygrsqllgavtslknngiqvygdvnmhkaggadtemnav	120	
Qy	121 EVNSRNRNOETISGEYTIEAWTKFDPGPGRGNTHSNPKWRMYHFGDTWDQSROLQNKIYKF	180	
Db	121 evnrsnrnqeisgeytieawktkdfpgrgnthsnfkwrwyhfgdtwdqdsrqlnkiykff	180	
Qy	181 RGTGKADWEVDIENGNDYLIMYADI DMHDHEVINELRNWGWWYINTLNLDGFRIDAVKH	240	
Db	181 rgtgkawdewediengnydylymadi dmhdhevinelrnwgyyntlnldgfriidavkh	240	
Qy	241 IKYSYTRDWLTGHVRNTTGKPFVAFAEFWKNDLAAIENLYNKTWSNHVSFDVPDLHYNLNA	300	
Db	241 ikysytrdwltghvrnttgkpfavaefwkndlaalenlynktswnhsfvdpvlhylnyna	300	
Qy	301 SNSGGYDFMRNILNGSVVQKHPITHAVTFVDNHDSOGPEALSFVQSWFKPLAYAILTLTRE	360	
Db	301 snsggymdmrnilngsvvqkhpithavtfvdnhdspgealesfvqswfkplayailtltre	360	

```
QY 361 QGYPVSFYGDYGYGIPTHGVPSMKSIDPILLQARQTYAYGTQHDYDFDHHDIIGWTRGDSS 420
|||||
Db 361 qgypsvfygdygygipthgvpsmksidpillaqrtaygtqhdyfddhdiigwtrgdss 420
|||||
QY 421 HPSNGSLATMSDGPCKWYVCKHKGAGVWRDITGNRSCTVTINADGKGNFTVNGGAVS 480
|||||
Db 421 hpsnglatmsdgpckwmyvgkhkagvwrdditnrgstvtinadgwnftvnggavs 480
|||||
QY 481 VVVKQ 485
|||||
Db 481 vvvkq 485
|||||

RESULT 3
AAB35714
ID AAB35714 standard; protein; 516 AA.
XX
AC AAB35714;
XX
DT 19-FEB-2001 (first entry)
XX
DE Mutant alpha-amylase amino acid sequence.
XX
KW Alpha-amylase; detergent; Bacillus.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 297
FT /note= "Represented as Alu in the specification"
FT Misc-difference 335
FT /note= "Represented as Aly in the specification"
XX
PN JP2000245466-A.
XX
PD 12-SEP-2000.
XX
PF 25-FEB-1999; 99JP-0048213.
XX
PR 25-FEB-1999; 99JP-0048213.
XX
PA (KAOS ) KAO CORP.
XX
DR WPI; 2000-615143/59.
XX
DR N-PSDB; AAC66234.
XX
PT A novel mutant alpha-amylase for use in a detergent composition -
XX
PS Claim 1; Page 5-6; 12pp; Japanese.
XX
CC The present invention relates to a mutant alpha-amylase. Included in the
CC invention are a gene encoding the mutant alpha-amylase, a vector
CC containing the gene, and a transformed cell recombinant by the vector. The
CC enzyme is used in a detergent composition. The present sequence
CC represents the mutant alpha-amylase protein.
XX
SQ Sequence 516 AA;

Query Match 99.5%; Score 2700; DB 21; Length 516;
Best Local Similarity 99.6%; Pred. No. 5.2e-218;
Matches 483; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWHLPNQDGNHNRRLRDAANLKSIGITAYWIPPAWKGTSONDVGGA 60
Db 32 hngtngtmmqyfewhlpnqdnhnrlddaanlksigitaywippawkgtsqndvgga 91
QY 61 YDLYDLGEFNQKGTVRTKYGTSQLOQAVTSLKNNGIQYGVVMMNHKGAGDGTENVAV 120
Db 92 ydlydlgefnqkgtvrtkysqlgavtslnkngiqygvvmmnhkgagdgtemnav 151
QY 121 EVNRNRNQEISGEYTEAWTKFDFCRGNTSHSNFKRWYHFDGTQDQSRQLQNKIYKF 180
|||||
```

```
Db 152 evnrnrnqeisgeyteawtkfdfpgrgnthsnfkwrwyhfdgtdwdqsrqlqnkiykf 211
QY 181 RGTGKAWDEVDLENGNYDYLMYADIDMDRPEVINELRNNGVWYTTNLNDGFRIDAVKH 240
|||||
Db 212 rtgkawdewvdiengnydylymyadidmdrpevinelrnngvwyttntclnldgfridavkh 271
|||||
QY 241 IKYSYTRDMLTHVRNTTGKPMFAVEFWKNDLAAIENYLNKTSWNHSHVFDVPLHYNLNA 300
|||||
Db 272 ikysytrdwlthvrnttgkpmfavafxkndlaaienylnktswnhshvfdvplhynlyna 331
|||||
QY 301 SNSGGYFDMRNILNGSVQKHPIHAVTFVDNHDHQGEALESFVQSKPLAYALILTRE 360
|||||
Db 332 snsggyfdmrnilngsvvqkphavtfvdnhdsgpealesfvqskplayallitre 391
|||||
QY 361 QGYPVSFYGDYGYGIPTHGVPSMKSIDPILLQARQTYAYGTQHDYDFDHHDIIGWTRGDSS 420
|||||
Db 392 qgypsvfygdygygipthgvpsmksidpillaqrtaygtqhdyfddhdiigwtrgdss 451
|||||
QY 421 HPSNGSLATMSDGPCKWYVCKHKGAGVWRDITGNRSCTVTINADGKGNFTVNGGAVS 480
|||||
Db 452 hpsnglatmsdgpckwmyvgkhkagvwrdditnrgstvtinadgwnftvnggavs 511
|||||
QY 481 VVVKQ 485
|||||
Db 512 vvvkq 516
|||||

RESULT 4
AAW31499
ID AAW31499 standard; protein; 485 AA.
XX
AC AAW31499;
XX
DT 08-APR-1998 (first entry)
XX
DE Bacillus sp. alpha amylase.
XX
KW Alpha-amylase; hard surface cleaning; dishwashing; laundry.
XX
OS Bacillus sp.
XX
PN WO9732961-A2.
XX
PD 12-SEP-1997.
XX
PF 04-MAR-1997; 97WO-US03635.
XX
PR 07-MAR-1996; 96WO-US03276.
XX
PA (PROC ) PROCTER & GAMBLE CO.
XX
PI Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S;
PI Showell MS, Ward G;
XX
DR WPI; 1997-457524/42.
XX
PT Detergent compositions for hard surface cleaning and laundry use -
PT contains Bacillus derived alpha amylase with improved
PT thermostability, reduced calcium ion dependency etc.
XX
PS Claim 1; Pages 86-87; 97pp; English.
XX
CC The present sequence is a Bacillus sp. alpha amylase with a
CC specific activity at least 25% higher than that of Termamyl (RTM)
CC at 25 to 55 degrees C at pH 8 to 10, measured by the Phadebas (RTM)
CC activity test. It is of use in hard surface cleaning, hand or
CC machine dishwashing and laundry at a temperature of 10 to 25
CC degrees C. Improved cleaning, stain removal and fabric care
CC obtained by using it at a concentration of 0.00018 to 0.06%
XX
SQ Sequence 485 AA;
```

Query Match 96.3%; Score 2613; DB 18; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGSQNDVGGA 60  
 DB 1 hhgctngtmmqyfewyfpndgnhnrirdaanksgitavwippawkgsgndvgga 60

QY 61 YDLXDLGFEFNQKGVTRTKYGRSLOQAVTSLKNGIQVYGDVVMNHKGGADGTEMNAV 120  
 DB 61 ydldxdlgfefnqkgvtrtkygrsloqavtslkngiqvygdvvmnhkggadgteivnav 120

QY 121 EVNRSNRNQEISGEYTTAEATKFDPPGRGNTHSNPKRWYHFDGTDWDQSRQLQNKIYKF 180  
 DB 121 evnrsnrnqetsgeyaekfddpgrgnthsnpkwnhfdgtdwdqsrqlqnkiykf 180

QY 181 RGTGKAWDEWDIENGNYDYLMDADIDMDHPEVINELRNMGVWYTNLTLDGFRIDAVKH 240  
 DB 181 rgtgkawdewdengnydyldmdadidmdhpevinelrnmgvwytnltldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAEFKNDLAAIENYLNKTSWNHVSFVPLHYNLYNA 300  
 DB 241 ikysftrdmlthvtrnttgkpmfavaefwkndlgaenlynktswnhsvfplhynlyna 300

QY 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSPQGEALSFVQSFKPLAYALILTRE 360  
 DB 301 snsggyydmrnilngsvvqkhphtavtfvndhdsqgealesfvqsfkplayaliltre 360

QY 361 QGYPSVFYGDYIGIPTHGVPSMSKIDPLQAROTYAGTQHDYFDHDDIIGWTRREGDSS 420  
 DB 361 qgypsvfgydyigipthgvpamkskidplqarctfaygtqhdvfdhddiigwtrreguss 420

QY 421 HPNSGLATIMSDGPGGNKMWYGVKHKAGQVWRDITGNRSQVTTINADGWNFTVNGGAVS 480  
 DB 421 hpnsglatimsdpggnkwmvygkagqvwrditgnrtgtvtinadgwnfsvnggsvs 480

QY 481 VWVKQ 485  
 DB 481 vvvkq 485

RESULT 5  
 AA48260  
 ID AA48260 standard; protein; 485 AA.  
 XX AC AA48260;  
 XX DT 02-JUL-1998 (first entry)  
 XX DE Bacillus sp. alpha amylase protein #1.  
 XX Alpha amylase; stain digestion; detergent; fabric laundry performance.  
 XX Bacillus sp.  
 XX OS WO9805748-A1.  
 XX PN 12-FEB-1998.  
 XX PD 01-AUG-1996; 96WO-US12612.  
 XX PF 01-AUG-1996; 96WO-US12612.  
 XX PR (PROC ) PROCTER & GAMBLE CO.  
 XX PA Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S;  
 XX PI Showell MS;  
 XX PT WPI; 1998-159168/14.  
 XX Use of specific alpha-amylase enzymes - in laundry detergent  
 PT compositions to provide effective cleaning and whitening of dingy  
 PT fabrics

XX Claim 1; Page 69-70; 82pp; English.  
 XX This sequence represents an alpha amylase from Bacillus sp. which is  
 CC used in a laundry detergent. The detergent compositions can be used  
 CC for boosting fabric laundry performance or for dingy  
 CC fabric cleanup.  
 XX SQ Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 19; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNDGNHNRRLRDDAANKSGITAVWIPPAWKGSQNDVGGA 60  
 DB 1 hhgctngtmmqyfewyfpndgnhnrirdaanksgitavwippawkgsgndvgga 60

QY 61 YDLXDLGFEFNQKGVTRTKYGRSLOQAVTSLKNGIQVYGDVVMNHKGGADGTEMNAV 120  
 DB 61 ydldxdlgfefnqkgvtrtkygrsloqavtslkngiqvygdvvmnhkggadgteivnav 120

QY 121 EVNRSNRNQEISGEYTTAEATKFDPPGRGNTHSNPKRWYHFDGTDWDQSRQLQNKIYKF 180  
 DB 121 evnrsnrnqetsgeyaekfddpgrgnthsnpkwnhfdgtdwdqsrqlqnkiykf 180

QY 181 RGTGKAWDEWDIENGNYDYLMDADIDMDHPEVINELRNMGVWYTNLTLDGFRIDAVKH 240  
 DB 181 rgtgkawdewdengnydyldmdadidmdhpevinelrnmgvwytnltldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAEFKNDLAAIENYLNKTSWNHVSFVPLHYNLYNA 300  
 DB 241 ikysftrdmlthvtrnttgkpmfavaefwkndlgaenlynktswnhsvfplhynlyna 300

QY 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSPQGEALSFVQSFKPLAYALILTRE 360  
 DB 301 snsggyydmrnilngsvvqkhphtavtfvndhdsqgealesfvqsfkplayaliltre 360

QY 361 QGYPSVFYGDYIGIPTHGVPSMSKIDPLQAROTYAGTQHDYFDHDDIIGWTRREGDSS 420  
 DB 361 qgypsvfgydyigipthgvpamkskidplqarctfaygtqhdvfdhddiigwtrreguss 420

QY 421 HPNSGLATIMSDGPGGNKMWYGVKHKAGQVWRDITGNRSQVTTINADGWNFTVNGGAVS 480  
 DB 421 hpnsglatimsdpggnkwmvygkagqvwrditgnrtgtvtinadgwnfsvnggsvs 480

QY 481 VWVKQ 485  
 DB 481 vvvkq 485

RESULT 6  
 AA48260  
 ID AA48260 standard; protein; 485 AA.  
 XX AC AA48260;  
 XX DT 27-AUG-1999 (first entry)  
 XX DE Bacillus sp. alpha-amylase protein fragment 1.  
 XX Alpha-amylase; cleaning composition; protease variant; spot removal;  
 KW detergent composition; hard surface cleaning; fabric cleaning;  
 KW dishwashing composition; oral cleaning composition; personal cleansing;  
 KW stain removal; soil removal; whiteness maintenance; dingy cleanup;  
 KW film removal.  
 XX OS Bacillus sp.  
 XX WO9920723-A2.  
 XX 29-APR-1999.



XX PF 23-OCT-1998; 98WO-US222486.  
 XX PR 23-OCT-1997; 97US-0956564.  
 XX PR 23-OCT-1997; 97US-0956323.  
 XX PR 23-OCT-1997; 97US-0956324.  
 XX PA (PROC ) PROCTER & GAMBLE CO.  
 XX PI Baek AC, Busch A, Ghosh CK, Ohtani R, Showell MS;  
 XX DR WPI; 1999-404706/34.  
 XX PT New cleaning compositions  
 XX PS Claim 1b(ii); Page 164-165; 169pp; English.  
 XX CC This invention describes novel cleaning compositions which contain a  
 CC protease variant with an amino acid substitution corresponding to  
 CC position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant.  
 CC The compositions can be used in e.g. detergent compositions, for cleaning  
 CC hard surfaces or fabrics, dishwashing compositions, oral cleaning  
 CC compositions, detergent cleaning compositions and personal cleansing  
 CC compositions. The combination of protease variants and alpha-amylase  
 CC variants in cleaning compositions can provide improved and enhanced  
 CC cleaning ability, including stain and/or soil removal and/or reduction  
 CC and/or whiteness maintenance and/or dingy cleanup and/or spot and/or  
 CC film removal and/or reduction, over conventional enzyme-containing  
 CC cleaning compositions.  
 XX Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLDDAANKLSKGITAVWIPPAWKGTSONDVGCGA 60  
 DB 1 hngtngtmmqyfewylpndgnhnrlddaanlkskgitavwippawkgtsqndvggga 60  
 QY 61 YDLYDLGEFNQKGTVRTKYGTSRQLOGAVTSLKNNGIQVYGVDMVNMHKGADGTEMVNAV 120  
 DB 61 yldylgefnqgtvrtkygtrnqlqaavtslknngiqvgdvmmhkggadgteivnav 120  
 QY 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTQDQSRQLOKNIYKF 180  
 DB 121 evnrsnrnqetsgeyaaleawtkfdfpgrgnhssfkwyhfdgtwdgsrqlqnkiyxf 180  
 QY 181 RGTGKAWMEVDIENGNDYLMYADIDMDHPEVINELRNWGVWYTNLNLDFRIDAVKH 240  
 DB 181 rgtgkawevedtengndylymyadvdmhpevihelrnwgvwytnlnldgfridavkh 240  
 QY 241 IKYSYTRDLTHTVRNTGKPMFAVEAFKNDLAAIENYLNKTSWNHVSFDPVPLHYLYNA 300  
 DB 241 ikysytrdlwthvrntgkpmfaveafkndlgalenylnktswnhsvfdvplhylyna 300  
 QY 301 SNSGGYFDMRNILNGSVQKHPTHAVTFVDNHDSPQGEALSFVQSWFKPLAYALILTRE 360  
 DB 301 snsggydmrnlnngsvqkphthavtfvdmhdsqpgealesfvqswfklpayalvltre 360  
 QY 361 QGYPSVFGDYGYGIPHGVPMSKSIDPLLQARQTYAYGTQHDYFDHDIIGWTREGDSS 420  
 DB 361 qgypsvfygdygygipchypamksidpllqarqtaygtqhdylfddhdiigwtregss 420  
 QY 421 HPSGLATIMSDGPGCKNMYCKKAGQVWRDITGNRSCTVTINADGNGFTVNGGAVS 480  
 DB 421 hpsglatimsdpgpgknmygknkagqvwrditgnrtgtvtinadgngftsvnggavs 480  
 QY 481 VVVKQ 485  
 DB 481 vvvkq 485

RESULT 7  
 AAY15415  
 ID AAY15415 standard; protein; 485 AA.  
 XX AC AAY15415;  
 XX DT 22-JUL-1999 (first entry)  
 XX DE Bacillus strain NCIB 12512 alpha-amylase protein.  
 XX KW Termamyl-like; alpha-amylase; variant; washing; dishwashing;  
 KW production; sweetener; ethanol; starch; textile desizing;  
 KW starch liquefaction; saccharification process.  
 XX OS Bacillus sp.  
 XX PN WO9923211-A1.  
 XX PD 14-MAY-1999.  
 XX PF 30-OCT-1998; 98WO-DK00471.  
 XX PR 14-JUL-1998; 98DK-0000936.  
 XX PR 30-OCT-1997; 97DK-0001240.  
 XX PA (NOVO ) NOVO-NORDISK AS.  
 XX PI Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;  
 PI Nissen TL, Svendsen A;  
 XX WPI; 1999-326987/27.  
 XX New Termamyl-like alpha-amylase variants  
 PS Claim 38; Page 77-79; 115pp; English.  
 CC The specification describes termamyl-like alpha-amylase variants that  
 CC have altered amino acid sequences to improve properties. The variants  
 CC are produced by creating one or more of the following mutations in  
 CC amino acid sequence of the parent termamyl-like alpha-amylase: T141,  
 CC K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183,  
 CC G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168,  
 CC Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273,  
 CC A274, L275, K311, E346, K385, G456, K458, P459, G460, T461, V462,  
 CC T463. The variants can be used for washing and/or dishwashing. They can  
 CC also be used in the production of sweeteners and ethanol from starch,  
 CC and/or for textile desizing, and in starch liquefaction and/or  
 CC saccharification processes. The present amylase can function as the  
 CC parent sequence in the production of the variants of the invention.  
 XX Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 HNGTNGTMMQYFEWHLPNNDGNHNRRLDDAANKLSKGITAVWIPPAWKGTSONDVGCGA 60  
 DB 1 hngtngtmmqyfewylpndgnhnrlddaanlkskgitavwippawkgtsqndvggga 60  
 QY 61 YDLYDLGEFNQKGTVRTKYGTSRQLOGAVTSLKNNGIQVYGVDMVNMHKGADGTEMVNAV 120  
 DB 61 yldylgefnqgtvrtkygtrnqlqaavtslknngiqvgdvmmhkggadgteivnav 120  
 QY 121 EVNRSNRNOEISGEYTIKAWTKFDFPGRGNTHSNFKRWYHFDGTQDQSRQLOKNIYKF 180  
 DB 121 evnrsnrnqetsgeyaaleawtkfdfpgrgnhssfkwyhfdgtwdgsrqlqnkiyxf 180  
 QY 181 RGTGKAWMEVDIENGNDYLMYADIDMDHPEVINELRNWGVWYTNLNLDFRIDAVKH 240  
 DB 181 rgtgkawevedtengndylymyadvdmhpevihelrnwgvwytnlnldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSDVDFVPLHYNLYNA 300  
 Db 241 ikysfrtdlthvrtnttgkpmfavaefwknldgalenylnktswnhsvdfvplhynlyna 300  
 QY 301 SNSGGYFDMRNILNGSVVQKHPIHATVFDVNDHSDQGEALSFVQSWFKPLAYALILPRE 360  
 Db 301 snsnggydmrnlngsvvqkhpithatvfdvndhsgpgealesfvqswfkplayalilpre 360  
 QY 361 QGYPSVFYGDYGIPTGHPVPSKMSKIDPLQARQTYAYCTQHDYFDHDDIIGWTREGDSS 420  
 Db 361 qgypsvfgydygiptghvpamkskidpllqarctfaygtqhdyfddhddilgwtregdss 420  
 QY 421 HPNSGLATIMSDGPGGNKMYVYGVKHKAGQVWRDITGNRSQGTVTINADGNGNFTVNGGAVS 480  
 Db 421 hpnsghatimsdpgpgnkmvyygknagqvwrditgnrtgtvtinadgngnftvnggavs 480  
 QY 481 VVWKQ 485  
 Db 481 vvwkq 485

## RESULT 8

AAAY15421 standard; protein; 485 AA.

AC AAAY15421;

DT 22-JUL-1999 (first entry)

DE Termamyl-like alpha-amylase protein.

KW Termamyl-like; alpha-amylase; variant; washing; dishwashing;

KW production; sweetener; ethanol; starch; textile desizing;

XX starch liquefaction; saccharification process.

OS Bacillus sp.

PN WO9923211-A1.

XX 14-MAY-1999.

PF 30-OCT-1998; 98WO-DK00471.

PR 14-JUL-1998; 98DK-0000936.

PR 30-OCT-1997; 97DK-0001240.

FA (NOVO ) NOVO-NORDISK AS.

PI Andersen C, Borchert TV, Kjaerulff S, Nielsen BR;

PI Nissen TL, Svendsen A;

DR WPI; 1999-326987/27.

XX New Termamyl-like alpha-amylase variants

PS Claim 38; Page 88-89; 115pp; English.

CC The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F367, W268, K269, N270, D271, L272, G273, A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present amylase can function as the parent sequence in the production of the variants of the invention.

XX Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEHPLNDGNHNRLLRDDAANKLSKIGTAVWIPPAWKGTSQNDVGGA 60  
 Db 1 hhngtngtmmqyfehplndgnhnrllrddaanlkskigtavwippawkgsqndvgga 60  
 QY 61 YDLXDLGFEFGKGTVRTKYGTRSQLOGAVTSLKNNIGIOVYGVVNNHKGAGDGTENVNAV 120  
 Db 61 ydlxdlgfefgkgtvrtkygtrnqlqaavtslkngiqvygvdvnnhkggagdtainnav 120  
 QY 121 EVNRSNRNOEJSGEYTBKATKFDGPGRGNTSHNPKRWYHFDGTDQSQLOLNKIKYKF 180  
 Db 121 evnrsnrnqetsgeyaieawtkfdpggrgnhssfkwrwyhfdgtdqsrqlgnkiykf 180  
 QY 181 RGTGKANDWEVDIENGNYDLYMAYADIDMDHPEVINELRNMGVWYTNLTNLDGFRIDAVKH 240  
 Db 181 rgtgkandwevdtengnydylmyadvdmhpeviheirnwgyvtyntlnlogfridavkh 240  
 QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSDVDFVPLHYNLYNA 300  
 Db 241 ikysfrtdlthvrtnttgkpmfavaefwknldgalenylnktswnhsvdfvplhynlyna 300  
 QY 301 SNSGGYFDMRNILNGSVVQKHPIHATVFDVNDHSDQGEALSFVQSWFKPLAYALILPRE 360  
 Db 301 snsnggydmrnlngsvvqkhpithatvfdvndhsgpgealesfvqswfkplayalilpre 360  
 QY 361 QGYPSVFYGDYGIPTGHPVPSKMSKIDPLQARQTYAYCTQHDYFDHDDIIGWTREGDSS 420  
 Db 361 qgypsvfgydygiptghvpamkskidpllqarctfaygtqhdyfddhddilgwtregdss 420  
 QY 421 HPNSGLATIMSDGPGGNKMYVYGVKHKAGQVWRDITGNRSQGTVTINADGNGNFTVNGGAVS 480  
 Db 421 hpnsghatimsdpgpgnkmvyygknagqvwrditgnrtgtvtinadgngnftvnggavs 480  
 QY 481 VVWKQ 485  
 Db 481 vvwkq 485

## RESULT 9

AAAY07381  
 ID AAAY07381 standard; Protein; 485 AA.

XX AC AAAY07381;

DT 16-JUL-1999 (first entry)

XX Wild type Termamyl(RTM)-like alpha-amylase protein #1.

DE Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;

KW dishwashing; laundry; textile; desizing; starch liquefaction;

KW sweetener; ethanol.

XX Bacillus sp.

OS Key Location/Qualifiers

XX Misc-difference 181.184

FT /note= "optionally 1, 2, 3 or all residues are deleted"

FT Misc-difference 195

FT /note= "optionally altered to any amino acid except an Asn residue"

FT Misc-difference 206

FT /note= "optionally altered to any amino acid except a Val residue"

FT Misc-difference 212

FT /note= "optionally altered to any amino acid except a Glu residue"

FT Misc-difference 216

FT /note= "optionally altered to any amino acid"

FT

FT

FT

FT

FT Misc-difference 269 except a Glu residue\*  
FT /note= \*optionally altered to any amino acid  
FT except a Lys residue\*  
XX

PN WO9919467-A1.

XX

PD 22-APR-1999.

XX

PF 13-OCT-1998; 98WO-DK00444.

XX

PR 13-OCT-1997; 97DK-0001172.

XX

PA (NOVO ) NOVO-NORDISK AS.

XX

PI Bisgard-Frantzen H, Borchert TV, Svendsen A;

XX

DR WPI; 1999-277632/23.

XX

XX Variant alpha-amylases - useful as detergents or for textile

PT desizing or starch liquefaction

PT

PS Claim 1; Page 61-63; 93pp; English.

XX

CC This sequence represents the parent sequence for new variants of a  
CC parent Termamyl-like alpha-amylase with alpha-amylase activity. The  
CC variants comprise mutations in 2-6 regions/positions relative to an  
CC alpha-amylase from either of two Bacillus species in WO9526397,  
CC B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or  
CC Bacillus sp. #707. The alpha-amylase variants are detergent additives  
CC for use in detergents for dishwashing, manual or automatic laundry.  
CC The variants can also be used for textile desizing or starch  
CC liquefaction (e.g. for production of sweeteners or ethanol).

XX Sequence 485 AA;

SQ

Query Match 96.3%; Score 2613; DB 20; Length 485;  
Best Local Similarity 95.1%; Pred. No. 9.3e-211;  
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWHLPGNDGNHWRDLDDAANKSKGITAVWIPPAWKGTSONDVGCGA 60

DB 1 hngtngtmqyfewylpndgnhwnlrddaanlkskgitavwippawkgtsqndvggga 60

QY 61 YDLYDLGEFNOKGTVTKYGRSLOQAVTSLKNGGIQVYGVVMMHKGADGTEMVNAV 120

DB 61 ydlydlgefngkgtvtrtkygrtrnqlqaavtclknngiqvygvdvmmhkggagdclelnav 120

QY 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKNRWYHFDGTDWQSRQLQNKIYKF 180

DB 121 evnrsnrnqetsgeyaieawtkkdfpgrgnhssfkwrwyhfdgtwdqsrqlqnkikf 180

QY 181 RGTGKAWDNEVDIENGNYDLYMTADIMDHPVINELRNKGWVYTNLTNDGFRIDAVKH 240

DB 181 rgtgkawdewdvtengnydylmyadvdmhdhpeviheirnwgvwytnltndgfridavkh 240

QY 241 IKYSYTRDLTHVRNTTGKPMFAVAFKNDLAAIENYLNKTSWNHSDVDFPLHYLYNA 300

DB 241 ikysfrdlthvrntctgkpmfavaefwkndlgalenylnktswnhsvdfvplhylyna 300

QY 301 SNSGGYDFMRNLGWSVQKHPIHAYTFVDNHDSPQGEALSFQSWFKPLAYALITRE 360

DB 301 snsnggydfmrnlngsvqkhphtavtfvndhdsqpgealesfvqwfplayalvtre 360

QY 361 QGYPSVFYGDYIGIPHGVPMSKSIDPLQARQTYAYGTQHDYDFDHDHDIIGTREGDSS 420

DB 361 qgypsvfgydyigipchgypamskidlplqarqtfaigtqdyfhdhdiigvtregns 420

QY 421 HPNSGLATIMSDPGGNKMYVCKKHAGQVWRDITGNRSCTVTINADGKGNFTVNGGAVS 480

DB 421 hpnsglatimsdpgpgnkmvygknkagqvrwditgnrtgtvtinadgwnfnsvnggsvs 480

QY 481 VVVKQ 485

DB 481 vvvkq 485

RESULT 10

AAY07391

XX ID AAY07391 standard; Protein; 485 AA.

XX

AC AAY07391;

XX

DT 16-JUL-1999 (first entry)

XX

DE Wild type Termamyl(RTM)-like alpha-amylase protein #7.

XX

KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;

KW dishwashing; laundry; textile; desizing; starch liquefaction;

KW sweetener; ethanol.

XX

OS Bacillus sp.

XX

PN WO9919467-A1.

XX

PD 22-APR-1999.

XX

PF 13-OCT-1998; 98WO-DK00444.

XX

PR 13-OCT-1997; 97DK-0001172.

XX

PA (NOVO ) NOVO-NORDISK AS.

XX

PI Bisgard-Frantzen H, Borchert TV, Svendsen A;

XX

DR WPI; 1999-277632/23.

XX

XX Variant alpha-amylases - useful as detergents or for textile

PT desizing or starch liquefaction

PT

PS Disclosure; Page 72-74; 93pp; English.

XX

CC This sequence represents the parent sequence for new variants of a  
CC parent Termamyl-like alpha-amylase with alpha-amylase activity. The  
CC variants comprise mutations in 2-6 regions/positions relative to an  
CC alpha-amylase from either of two Bacillus species in WO9526397,  
CC B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or  
CC Bacillus sp. #707. The alpha-amylase variants are detergent additives  
CC for use in detergents for dishwashing, manual or automatic laundry.  
CC The variants can also be used for textile desizing or starch  
CC liquefaction (e.g. for production of sweeteners or ethanol).

XX

SQ Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 20; Length 485;

Best Local Similarity 95.1%; Pred. No. 9.3e-211;

Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWHLPGNDGNHWRDLDDAANKSKGITAVWIPPAWKGTSONDVGCGA 60

DB 1 hngtngtmqyfewylpndgnhwnlrddaanlkskgitavwippawkgtsqndvggga 60

QY 61 YDLYDLGEFNOKGTVTKYGRSLOQAVTSLKNGGIQVYGVVMMHKGADGTEMVNAV 120

DB 61 ydlydlgefngkgtvtrtkygrtrnqlqaavtclknngiqvygvdvmmhkggagdclelnav 120

QY 121 EVNRSNRNOEISGEYTIETAWTKFDFGCGNTHSNFKNRWYHFDGTDWQSRQLQNKIYKF 180

DB 121 evnrsnrnqetsgeyaieawtkkdfpgrgnhssfkwrwyhfdgtwdqsrqlqnkikf 180

QY 181 RGTGKAWDNEVDIENGNYDLYMTADIMDHPVINELRNKGWVYTNLTNDGFRIDAVKH 240

DB 181 rgtgkawdewdvtengnydylmyadvdmhdhpeviheirnwgvwytnltndgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAFWKNDAIAENYLNKTSWNHVSFVDFVPLHYNLYNA 300  
 Db 241 ikysftrdwlthvrnttgkpmfavaefwknldgaieenlylnktswnhsvfdvplhynlyna 300

QY 301 SNSGGYFDMRNILNGSVVQKHPITHAVTEVDNHDSDQCEALESFVQSWFKPLAYALITRE 360  
 Db 301 snsggydmrnilngsvvqkhpithavtevdnhdsgcealesfvqswfkplayalvtre 360

QY 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHDDIIGWTRGDS 420  
 Db 361 qgypsvfgydygiptghgvpamskidpllqarqtfaigtqhdqfhdhdiigwtrgds 420

QY 421 HPNSGLATIMSDGPGGNKMYVGHKKGAGQVWRDITGNRGTVTINADGNGFTVNGGVS 480  
 Db 421 hpnsghlatimsdpggnkmyvghkkgagvwrtditgnrtgtvtinadgngftvnggsvs 480

QY 481 VWVKQ 485  
 Db 481 vwvkq 485

RESULT 11  
 AAY99602  
 ID AAY99602 standard; Protein; 485 AA.  
 AC AAY99602;  
 DT 04-SEP-2000 (first entry)  
 XX Bacillus parent Termamyl-like alpha-amylase #1.  
 XX Bacillus; alpha-amylase; washing; textile desizing;  
 KW starch liquefaction; saccharification; mutein; mutant;  
 KW enzyme stability; hybrid.  
 XX Bacillus sp.  
 XX WO200029560-A1.  
 XX 25-MAY-2000.  
 XX 16-NOV-1999; 99WO-DK00628.  
 XX 16-NOV-1998; 98DK-0001495.  
 XX (NOVO-) NOVO-NORDISK AS.  
 XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;  
 XX WPI; 2000-387777/33.  
 XX N-PSDB; AAA48480.  
 XX Variant of parent termamyl-like alpha amylase useful for washing,  
 PT textile desizing and starch liquefaction, comprising alterations in one  
 PT or more solvent exposed amino acid residues -  
 XX Claim 8; Page 53-54; 80pp; English.  
 XX The present sequence is a parent Termamyl-like alpha-amylase  
 CC from which mutants with increased stability at acidic pH, low calcium  
 CC concentration and high temperatures have been derived. The sequence  
 CC encoding this protein was isolated from a Bacillus genomic DNA library.  
 CC A variant may contain mutations in one or more solvent exposed amino  
 CC acid residues to increase the overall hydrophobicity of the enzyme or the  
 CC overall number of methyl groups in the side chains of exposed residues  
 CC may be increased. The mutations can be incorporated by site-directed  
 CC mutagenesis or by random mutagenesis. As a result of their increased  
 CC stability, the variants are suitable for the industrial processing of  
 CC starch, i.e. starch liquefaction and saccharification. They may also be  
 CC useful for washing, dishwashing and textile desizing. Hybrid  
 CC alpha-amylases comprising partial amino acid sequences derived from two  
 CC or more alpha-amylases have also been created in order to increase  
 CC enzyme stability.

XX SQ Sequence 485 AA;  
 Query Match 96.3%; Score 2613; DB 21; Length 485;  
 Best Local Similarity 95.1%; Pred. No. 9.3e-211;  
 Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEHLLNDGNHNRLLRDDAANLKSIGTAVWIPPAWKGTSONDVGYGA 60  
 Db 1 hngtngtmmqyfewllpndgnhnrllrddaanlksigtavwippawkgtsqndvgyga 60

QY 61 YDLYDLGFEFNOKGTVRTKYGTRSOLOQAVTSLKNGGIQVYGVVMNHKGGADGTEWNAV 120  
 Db 61 yldydlgfefnkgvtrtkygttrlnqlqaavtslknngliqvyygvvmnhkggadgteivnav 120

QY 121 EVNRSNRNQEISGEYTIKAWTKFDPGGRNTHSNFKRWYHFDGTDWDSROLQNKIYKF 180  
 Db 121 evnrsnrnqetsgeyaieawtkfdpggrgnhssfkwrwyhfdgtdwdsrqlqknkiykf 180

QY 181 RGTGKAWDEVDIENGNYDYLMIYADIDMDHPEVINELRNWGVWYTNLNLGDFRIDAVKH 240  
 Db 181 rgtgkawdewdteingnydyimydvdmdhpevinelnrgwvwytnlnldgfridavkh 240

QY 241 IKYSYTRDMLTHVRNTTGKPMFAVAFWKNDAIAENYLNKTSWNHVSFVDFVPLHYNLYNA 300  
 Db 241 ikysftrdwlthvrnttgkpmfavaefwknldgaieenlylnktswnhsvfdvplhynlyna 300

QY 301 SNSGGYFDMRNILNGSVVQKHPITHAVTFVDNHDSDQCEALESFVQSWFKPLAYALITRE 360  
 Db 301 snsggydmrnilngsvvqkhpithavtfvdnhdsgcealesfvqswfkplayalvtre 360

QY 361 QGYPSVFYGDYGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHDDIIGWTRGDS 420  
 Db 361 qgypsvfgydygiptghgvpamskidpllqarqtfaigtqhdqfhdhdiigwtrgds 420

QY 421 HPNSGLATIMSDGPGGNKMYVGHKKGAGQVWRDITGNRGTVTINADGNGFTVNGGVS 480  
 Db 421 hpnsghlatimsdpggnkmyvghkkgagvwrtditgnrtgtvtinadgngftvnggsvs 480

QY 481 VWVKQ 485  
 Db 481 vwvkq 485

RESULT 12  
 AAY99608  
 ID AAY99608 standard; Protein; 485 AA.  
 AC AAY99608;  
 DT 04-SEP-2000 (first entry)  
 XX Bacillus Termamyl-like alpha-amylase.  
 XX Bacillus; alpha-amylase; washing; textile desizing;  
 KW starch liquefaction; saccharification; mutein; mutant;  
 KW enzyme stability; hybrid.  
 XX Bacillus sp.  
 XX WO200029560-A1.  
 XX 25-MAY-2000.  
 XX 16-NOV-1999; 99WO-DK00628.  
 XX 16-NOV-1998; 98DK-0001495.  
 XX (NOVO ) NOVO-NORDISK AS.  
 XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;  
 XX PI

```
DR WPI; 2000-387777/33.
XX Variant of parent termamyl-like alpha amylase useful for washing,
PT textile desizing and starch liquefaction, comprising alterations in one
PT or more solvent exposed amino acid residues
XX
XX Claim 8; Page 62-64; 80pp; English.
XX
CC The present sequence is a parent alpha-amylase from which mutants
CC with increased stability at acidic pH, low calcium concentration and high
CC temperatures have been derived. The sequence encoding this enzyme was
CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of methyl
CC groups in the side chains of exposed residues may be increased. The
CC mutations can be incorporated by site-directed mutagenesis or by random
CC mutagenesis. As a result of their increased stability, the variants are
CC suitable for the industrial processing of starch, i.e. starch
CC liquefaction and saccharification. They may also be useful for washing,
CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
CC partial amino acid sequences derived from two or more alpha-amylases
CC have also been created in order to increase enzyme stability.
XX
SQ Sequence 485 AA;

Query Match 96.3%; Score 2613; DB 21; Length 485;
Best Local Similarity 95.1%; Pred. No. 9.3e-211;
Matches 461; Conservative 16; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNDGNHNRLLRDDAANKSKGITAVWIPPAWKTSQNDVGGA 60
DB 1 hngtngtmqyfewylpndgnhwnrlrddaanlkskgitavwippawkgtsqndvgga 60
QY 61 YDLYLGEFNGKQGTVRTKYGTRSQLOGAVTSLKNGGQVYGVVVMNHKGGADGTEMYNAV 120
DB 61 ydlylgefngkgtvrtkygtrnqlgaavtslknngiqvvgdvmmnhkkgadgteiynav 120
QY 121 EVNRSNRNQISGEYTTAEWTKFDFPGRGNTSHNFKRWYHFDGTDWDQSRQLQNKIYKF 180
DB 121 evnrsnrnqetsgeyaleavtkdfpgrgnnhsfkwrwyhfdgtdwdqsrqlqnklykf 180
QY 181 RGTGKAWDEVDENGNDYLYMADIDMDHPEVINELRNNGVWYTNPLNLDGFRIDAVKH 240
DB 181 rgtgkawdewdengndylymadvdmhpeviheirnwgvwytnplnldgfridavkh 240
QY 241 IKYSYTRDWLTHVRNTTGGKPMFAVEFKNDLAAIENYLNKTSNHSVDFVPLHYNLYNA 300
DB 241 ikysftrdwlthvrnttggkpmfavaefwknldgalienylnktswnhsvdfvplhynlyna 300
QY 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSPQGEALESFVQSWFKPLAYALILTRE 360
DB 301 snsnggydmrnlngsvvqkhphtavtfvndhsqgealesfvqgwkplayalvltre 360
QY 361 QGVPSPVGYGYGIPRHGVPSMSKIDPLQARQTYAYGQHDYFDHHDHIIGWTRREGDSS 420
DB 361 qgvpsvfygygygiprhgvpsmskidlqarqttyaygqhdyfddhhdhiiwgtrregss 420
QY 421 HPNSGLATINSDGGGKNWYVKGKAGQVWRDITGNRSCTVINADGWNFTVNGGAVS 480
DB 421 hpnsglatinsdgggknwvygkagqvwrditgnrtgtvtinadgwnfsvnggavs 480
QY 481 VVVKQ 485
DB 481 vvvkq 485

RESULT 13
ID AAW12113
XX AAW12113 standard; protein; 485 AA.
AC AAW12113;
XX
```

```
DT 08-APR-1997 (first entry)
XX Alpha-amylase variant L217I.
XX Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
KW calcium ion dependency; alpha-amylolytic activity; washing composition;
KW textile desizing; papermaking; beer-making; ethanol production;
XX sweetener.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 217
FT /label= L217I
XX
XX WO9623873-A1.
XX
XX 08-AUG-1996.
XX
XX 05-FEB-1996; 96WO-DK00056.
XX
XX 06-OCT-1995; 95DK-0001121.
XX 03-FEB-1995; 95DK-0000126.
XX 29-MAR-1995; 95DK-0000336.
XX 29-SEP-1995; 95DK-0001097.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Bisgard-frantzen H, Borchert T, Svendsen A;
XX
XX WPI; 1996-371423/37.
XX
XX Alpha-amylase variants - with improved thermal and oxidation
PT stability and reduced calcium ion dependency
XX
XX Claim 10; : l1ipp; English.
XX
XX AAW12098-W12144 represent alpha-amylase variants of the invention. The
CC variants of the invention were created using site directed, or random,
CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
CC represented by AAW12955, AAW12956, AAR81835 and AAR81836.
CC AAW12098-W12136, AAW12141, AAW12142 and AAW12144 are specifically
CC variants of the alkaphilic Bacillus strain NCIB 12512 alpha-amylase shown
CC in AAR81835. These variants can have improved thermal stability (such as
CC at temperatures in the range of 40-70 degrees Celcius), and/or oxidation
CC stability, and/or reduced calcium ion dependency. The variants can also
CC have increased alpha-amylolytic activity (especially at pH values in the
CC range of 8.5-10.5), and improved binding of a particular substrate.
CC These variant alpha-amylases also possess improved specificity to a
CC particular substrate, and/or improved specificity with respect to
CC cleavage of substrate. These sequences can be used in detergent and
CC washing compositions, and for textile desizing. The alpha-amylase
CC variants can also be used in papermaking and beer-making processes.
CC These variants can also be used in the production of sweeteners and
CC ethanol from starch.
XX
XX Sequence 485 AA;

Query Match 96.2%; Score 2611; DB 17; Length 485;
Best Local Similarity 94.8%; Pred. No. 1.4e-210;
Matches 460; Conservative 17; Mismatches 8; Indels 0; Gaps 0;

QY 1 HHNGTNGTMMQYFEWHLPNDGNHNRLLRDDAANKSKGITAVWIPPAWKTSQNDVGGA 60
DB 1 hngtngtmqyfewylpndgnhwnrlrddaanlkskgitavwippawkgtsqndvgga 60
QY 61 YDLYDLGEFNGKQGTVRTKYGTRSQLOGAVTSLKNGGQVYGVVVMNHKGGADGTEMYNAV 120
DB 61 ydlylgefngkgtvrtkygtrnqlgaavtslknngiqvvgdvmmnhkkgadgteiynav 120
QY 121 EVNRSNRNQISGEYTTAEWTKFDFPGRGNTSHNFKRWYHFDGTDWDQSRQLQNKIYKF 180
DB 121 evnrsnrnqetsgeyaleavtkdfpgrgnnhsfkwrwyhfdgtdwdqsrqlqnklykf 180
```

Db 121 evnsnrnqetsgeyaieawtkfpgprgnhssfkwrwyhfdgtwdqsrqlgnkiykf 180  
 Qy 181 RGTGKAWDEYDIENGNYDLYMADIDMDHPVINELRNMGWYNTNTLNLGDFRIDAVKH 240  
 Db 181 rgtgkawdevdtengnydylmadvdmhpeviheirngvwyntntlnldgfridavkh 240  
 Qy 241 IKYSYTRDLWTHVRNTTKPMFAVAEFKNDLAAIENYLNKTSWNHSDVDFPLHYNLYNA 300  
 Db 241 ikysftrdwlthvnrnttkpmafavaefwkndlgalenylnktswnhsvfdvplhynlyna 300  
 Qy 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSDPGALESFVQSWFKPLAYAILTIRE 360  
 Db 301 snsggymrnilngsvvqkhphtavtfvdndhspqaleesfvqwkfpalayalvltre 360  
 Qy 361 QGYPSVFYGYGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHHDIIIGWTREGDSS 420  
 Db 361 qgypsvfygygyipthgvpamksidpllqarqtaygtqhdtyfdhhdiiigwtregss 420  
 Qy 421 HPNSGLATIMSDGPGGNKMYVGHKAGQVWRDITGNRSQVTVTINADGWGNTVNGGAVS 480  
 Db 421 hpnsghlatimsdpgpgnkmvghkagqvwrdrtnrsgtvtinadgwgntsvnggsvs 480  
 Qy 481 VWVKQ 485  
 Db 481 vvwkq 485

RESULT 14  
 AAW12129  
 ID AAW12129 standard; protein: 485 AA.  
 XX AC AAW12129;  
 XX DT 08-APR-1997 (first entry)  
 XX DE Alpha-amylase variant E190Q.  
 XX KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;  
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;  
 KW textile desizing; papermaking; beer-making; ethanol production;  
 KW sweetener.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 XX FT Misc-difference 190  
 XX FT /label= E190Q  
 XX PN W09623873-A1.  
 XX PD 08-AUG-1996.  
 XX PF 05-FEB-1996; 96WO-DK000056.  
 XX PR 06-OCT-1995; 95DK-0001121.  
 XX PR 03-FEB-1995; 95DK-0000126.  
 XX PR 29-MAR-1995; 95DK-0000336.  
 XX PR 29-SEP-1995; 95DK-0001097.  
 XX PA (NOVO ) NOVO-NORDISK AS.  
 XX PI Bisgard-frantzen H, Borchert T, Svendsen A;  
 XX DR WPI; 1996-371423/37.  
 XX PT Alpha-amylase variants - with improved thermal and oxidation  
 XX stability and reduced calcium ion dependency  
 XX PS Claim 11; ; 11lpp; English.  
 XX CC AAW12098-W12144 represent alpha-amylase variants of the invention. The  
 CC variants of the invention were created using site directed, or random,  
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases

CC represented by AAW12955, AAW12956, AAR1835 and AAR1836.  
 CC AAW12098-W12136, AAW12141, AAW12142 and AAW12144 are specifically  
 CC variants of the alkaliphilic Bacillus strain NCIB 12512 alpha-amylase shown  
 CC in AAR1835. These variants can have improved thermal stability (such as  
 CC at temperatures in the range of 40-70 degrees Celsius), and/or oxidation  
 CC stability, and/or reduced calcium ion dependency. The variants can also  
 CC have increased alpha-amylolytic activity (especially at pH values in the  
 CC range of 8.5-10.5), and improved binding of a particular substrate.  
 CC These variant alpha-amylases also possess improved specificity to a  
 CC particular substrate, and/or improved specificity with respect to  
 CC cleavage of substrate. These sequences can be used in detergent and  
 CC washing compositions, and for textile desizing. The alpha-amylase  
 CC variants can also be used in papermaking and beer-making processes.  
 CC These variants can also be used in the production of sweeteners and  
 CC ethanol from starch.  
 XX SQ Sequence 485 AA;  
 Query Match 96.2%; Score 2610; DB 17; Length 485;  
 Best Local Similarity 94.8%; Pred. No. 1.7e-210;  
 Matches 460; Conservative 17; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 HNGTNGTMMOYFEWHLPPNDGNHWNRLRDDAANKLSKGITAVWIPPAWKGTSONDVGYGA 60  
 Db 1 hngtngtmmdyfewipndgnhwnrlrddaanlkskgitavwippawkwgtsndvgyga 60  
 Qy 61 YDLXDLGEFNQKGTVRTKYGRSLOLQGAVTSLKNNGIQVYGVVNMHKGADGTEMVNAV 120  
 Db 61 ydylxlgefnqkgtvrtkygrnqlqaavtslknngiqvgygvnmhkggadgteivnav 120  
 Qy 121 EVNSNRNQEISGEYTTAEATKFDPPGRGNTHSNFKRWYHFDGTDWDQSRQLQNKIYKF 180  
 Db 121 evnsnrnqetsgeyaieawtkfpgprgnhssfkwrwyhfdgtwdqsrqlgnkiykf 180  
 Qy 181 RGTGKAWDEYDIENGNYDLYMADIDMDHPVINELRNMGWYNTNTLNLGDFRIDAVKH 240  
 Db 181 rgtgkawdevdtengnydylmadvdmhpeviheirngvwyntntlnldgfridavkh 240  
 Qy 241 IKYSYTRDLWTHVRNTTKPMFAVAEFKNDLAAIENYLNKTSWNHSDVDFPLHYNLYNA 300  
 Db 241 ikysftrdwlthvnrnttkpmafavaefwkndlgalenylnktswnhsvfdvplhynlyna 300  
 Qy 301 SNSGGYFDMRNILNGSVVQKHPHIAVTFVDNHDSDPGALESFVQSWFKPLAYAILTIRE 360  
 Db 301 snsggymrnilngsvvqkhphtavtfvdndhspqaleesfvqwkfpalayalvltre 360  
 Qy 361 QGYPSVFYGYGIPTHGVPMSKSIDPLQARQTYAYGTQHDYFDHHDIIIGWTREGDSS 420  
 Db 361 qgypsvfygygyipthgvpamksidpllqarqtaygtqhdtyfdhhdiiigwtregss 420  
 Qy 421 HPNSGLATIMSDGPGGNKMYVGHKAGQVWRDITGNRSQVTVTINADGWGNTVNGGAVS 480  
 Db 421 hpnsghlatimsdpgpgnkmvghkagqvwrdrtnrsgtvtinadgwgntsvnggsvs 480  
 Qy 481 VWVKQ 485  
 Db 481 vvwkq 485

RESULT 15  
 AAW12130  
 ID AAW12130 standard; protein: 485 AA.  
 XX AC AAW12130;  
 XX DT 08-APR-1997 (first entry)  
 XX DE Alpha-amylase variant E194Q.  
 XX KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;  
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;  
 KW textile desizing; papermaking; beer-making; ethanol production;



**THIS PAGE BLANK (USPTO)**





51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67  
157 CAAATGATGATGGGTATGGAGCCTATGATCTTTATGATTAGGGGAAT 206  
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84  
207 TAATCAAAAGGGGCGGTTCGTACTTAAGTATGGGACACGTAGTCAAT 256  
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrClyAsp 100  
257 AGTCGTGCATCCATGCTTTAAGATAATAGCGTTCAAGTTATGGGGAT 306  
101 ValValMetAsnHisLysMetClyAlaAspPheThrGluAlaValGlnAl 117  
307 GTAGTGATGAACCAATAAAGGAGGAGCTGATGCTACAGAAAACGTTCT 356  
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134  
357 TGTGAGGTGAATCAATAACCGGAATCAAGAAATATCTGGGAGCTACA 406  
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150  
407 CAATGAGCTTGGACTAAGTTTATGATTTCCAGGAGGGGTAAATACAT 456  
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167  
457 TCAGACTTTAAATGGCGTGTGATATCATTTCCGATGCTAGATTGGATCA 506  
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181  
507 ATCAGCAATTCCAAAATCGTACTACAAATCCGAGGTGATGGTAAG 556  
182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197  
557 CATGGGATGGGAAGTAGATTCGAAAATGAAATATGATTTAATG 606  
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214  
607 TATCCAGATGATAGTATGATATCCCGAGGTAGTAAATGAGCTTAGAAG 656  
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231  
657 ATGGGAGAATGGTATACAAATACATTAATCTTGATGATTTAGGATCG 706  
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247  
707 ATGGGTGAAGCATATTAATAATAGCTTTACACGTGATGTTGACCCAT 756  
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrp 264  
757 GTAAGAAACCAACGGGAAAGAAATGTTGCTGTTGCTGAATTTGGAA 806  
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGlu 281  
807 AAATGATTTAGTGCCTTGGAGAACTATTAAATAAAACAAACGTAATC 856  
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297  
857 ATCTGCTTGTATGCTCCCTTCATTAATATCTTTATACGCGGTCAAT 906  
298 GlnGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314  
907 AGTGGAGCAACTATGACATGGCAAACTCTTAATGGAACGGTTGTTCA 956  
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331  
957 AAGCATCAATGATCGCGTAACTTTTGTGATATACGATTCGATCAAC 1006  
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347  
1007 CTGGGGAATCATTAGATCATTTGTACAGAAGATGTTTAAGCCACTTGT 1056

348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrG 364  
1057 TATCGGCTTATTTAAACAAGAGAAAGGCTATCCCTCTCTCTCTATGG 1106  
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381  
1107 TGACTACTATGAATTCACACACATATGTGCTCCAGCAATGAAGCCAGA 1156  
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397  
1157 TTGATCAATCTTAGAGCGCGTCAAAATTTTGCATATGGAACACAACAT 1206  
398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414  
1207 GATATTTTACCATCATATAATATGCGATGGACACGCTGAAGGAAATAC 1256  
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431  
1257 CAGCATCCCAATTCAGGACTTCGACTATCATGTCGGATGGCCAGGG 1306  
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447  
1307 GAGAGAAATGGATGTAGTAGGCGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356  
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464  
1357 GACATACTGGAATAAACCCAGCAACAGTTACGATCAATGCAGATGGATG 1406  
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480  
1407 GGCTAATTTTCAATAATGGAGGATCTGTTCCATTTGGTGAACGA 1455  
seq\_name: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-861-837-5  
seq\_documentation\_block:  
; Sequence 5, Application US/08861837  
; Patent No. 5856164  
; GENERAL INFORMATION:  
; APPLICANT: Ottrup, Helle  
; APPLICANT: Bisgaard-Frantzen, Henrik  
; APPLICANT: Ostergaard, Peter Rahbek  
; APPLICANT: Rasmussen, Michael Dolberg  
; APPLICANT: Van Der Zee, Pia  
; TITLE OF INVENTION: Alkaline Bacillus Amylase  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5856164o No. 5856164disk of No. 5856164th America  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,837  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/446,803  
; FILING DATE: 01-June-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harrington, James J.  
; REGISTRATION NUMBER: 38,711  
; REFERENCE/DOCKET NUMBER: 4157,204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 867-0123  
; TELEFAX: (212) 878-9655  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-861-837-5

alignment_scores:
  Quality: 1860.50      Length: 483
  Ratio: 4.327          Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

alignment_block:
US-09-590-375-1 x US-08-861-837-5 ..
Align seg 1/1 to: US-08-861-837-5 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
7 AATGGACAATGGGACGATGATGCAATACTTTGAATGGCACTTGCTTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34
57 TGATGGGAATCACTGGATAGATTAAGAGATGATGCTAGTAATCTAAGAA 106
34 sAlaGlyIleThrAlaIleTrpPleProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATACCGCTATTGGATTCCGCCCTGGCTGGAAAGGACTTGC 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyLup 67
157 CAAATGATGATGGGTATGGAGCTATGATCTTTATGATTTAGGGCAATT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeu 84
207 TAAATCAAAAGGGGCGGTTCGTACTAAGTATGGGACACGTAGTCAATTGG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGTCGCCATCCATGCTTTAAGAATAATGGCGTTCAAGCTTTATGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGln 117
307 GTAGTGATGAACCAATAAGCAGGAGCTGATGCTACAGAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134
357 TGTCCAGGTGAATCCAAATCCGGAATCAAGAAATATCTGGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
407 CAATTGAGCTTGGACTAAGATTGATTTCCAGGGAGGGGTAATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAsp 167
457 TCAGACTTTAAATGGCGTTGGTATCATCTTCGATGCTAGATTGGGATCA 506
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 181
507 ATCAGACAATTCCAAAATCCGATCTACAAATTCGAGGTGATGGTAAGG 556
182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197
557 CATGGGATTGGGAAGTAGATTCCGAAATGGAAATATGATATTATTAAAG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLys 214
607 TATGCAGATGTAGATATGATCATCCGGAGGTAGTAATAGCTTAGAAG 656
214 prpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeu 231
657 ATGGGGAGAGATGGTATACAAATACATTAATCTTGTGATTTAGGATCG 706

```

```

231 sPAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATGCGGTGAACATATTAAATATAGCTTTACACGTGATTTGGTTGACCAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrp 264
757 GTAAGAAACGCAACGGGAAAGAAATGTTGCTGTTGCTGAATTTGGAA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGlu 281
807 AAATGATTTAGTGCTTGGAGAACATTTAAATAAACAACAACTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 ATCTGCTCTTGTATGTCCTTCATTAATCTTTATAACGCGTCAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuVal 314
907 AGTGGAGGCAACTATGACATGGCAAACTTCTTAATGGAACGGTTGTTCA 956
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGln 331
957 AAAGCATCAATGCATGCCGTAACTTTTGGATAATCACGATCTCAAC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
1007 CTGGGAATCATTAGAATCATTTGTACAAGATGGTTTAAGCCACTTGCT 1056
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyr 364
1057 TATGCGCTTATTTTAAACAAGAACAAAGCATCTCCCTCTGCTCTATGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMet 381
1107 TGACTACTATGGAATTCACACACATATGTGCCAGCAATGAAAGCCAGA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
1157 TTGATCCAATCTTAGAGCGCGTCAAAATTTGCATATGGAACACACAT 1206
398 AspTyrPheAspHisTrpAspValValGlyTyrTrpThrArgGlySer 414
1207 GATTTATTTGACCATCATATAATAATCGGATGGACACGTTGAAGAAAT 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGly 431
1257 CACGCATCCCAATTCAGGACTTCGACTATCATGTCGATGGGCCAGGG 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
1307 GAGAGAAATGGATGTACGTAGGCAAAATAAAGCAGTCAAGTTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGly 464
1357 GACATAACTGGAATAAACCAGGAACAGTATCAGCATCAATGCAGATGG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
1407 GGTAAATTTTCAGTAAATGGAGGATCTGTTCCATTTGGGTGAAACGA 1455

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-656-5
seq_documentation_block:
; Sequence 5, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:

```

22.

```

431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
|||||
1307 GAGAGAAATGGATGTACGTAGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
|||||
1357 GACATAACTGGAAATAAACACAGGAACAGTTACGATCAATGCAGATGGATG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
|||||
1407 GCCTAATTTTTCAGTAATAGGAGGATCGTTTCCATTTGGGTGAACGA 1455
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-10
seq_documentation_block:
; Sequence 10, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170.670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-10

```

```

alignment_scores:
  Quality: 1860.50      Length: 483
  Ratio: 4.327          Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

```

```
alignment_block:
```

```
US-09-590-375-1 x US-09-170-670-10 ..
```

```
Align seg 1/1 to: US-09-170-670-10 from: 1 to: 1455
```

```

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
|||||
7 AATGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTTGCTAA 56
17 naspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34
|||||
57 TGATGGGAATCACTGGAATAGATAAGAGATGATGCTAGTAATCTAAGAA 106
34 sPAAlaIleThrAlaIleTrpProAlaTyrLysGlyAsnSer 50
|||||
107 ATAGAGGTATACCGCTATTGGATTCCCGCTGCCCTGGAAAGGACTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
|||||
157 CAAATGATGTGGGGTATGGAGCTATGATCTTTATGATTAGGGGAATT 206
67 easnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
|||||
207 TAATCAAAAGGGGACGGTTTCGTACTAAGTATGGACACGTACTCAATTGG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
|||||
257 AGTCGCCATCCATCGCTTTAAGAATAATGGCGGTCAAGTTTATGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117

```

```

|||||
307 GTAGTGATGAACCAATAAAGGAGGAGCTGCTACAGAAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
|||||
357 TCTCGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
|||||
407 CAATTGAGCTTGGACTAAGTTTGTATTTCCAGGGAGGGGTAAATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
|||||
457 TCAGACTTTAAATGGCGTTGGTATCATCTTCGATGTTAGATTGGGATCA 506
167 nargTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 181
|||||
507 ATCAGACAAATCCAAATCGTATCTACAAATTCGAGAGTGATGGTAAGG 556
182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197
|||||
557 CATGGATTGGGAAGTAGATTCCGAAAATGGAATTTATGATTATTAAATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
|||||
607 TATGCAGATGTAGATATGCGATCATCGGAGGTAGTAAATGAGCTTAGAAG 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
|||||
657 ATCGGAGAAATGGTATACAAATACATTAATCTTGATGATTTAGGATCG 706
231 sPAAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
|||||
707 ATCGCGTGAAGCATATTAATATAGCTTTACACGTGATTTGGTTGACCCAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
|||||
757 GTAAGAAACGCAACGCGGAAAGAAATGTTTGTCTGCTGAATTTGGAA 806
264 saspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
|||||
807 AATGATTTAGGTGGCTTGGAGAACTATTAAATAAACAACAACTGGAAT 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
|||||
857 ATTCTGCTTTGATGTCCTTCATTATACTTTTAAACGGCTCAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl 314
|||||
907 AGTGGAGGCAACTATGACATGGCAAACTTCTTAATGGAACGGTTCTTCA 956
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlop 331
|||||
957 AAAGCATCAATGCGTACCTTAACCTTTTGGGATAATCACGATCTTCAAC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
|||||
1007 CTGGGAATCATTAGATCATTTGTACAAGATGGTTTAAGCCACTTGCT 1056
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl 364
|||||
1057 TATGCGCTTATTTTAAAGAGAACAAAGGCTATCCCTCTGCTTCTATGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
|||||
1107 TGACTACTATGGAATTCACACACATAGTGTCCAGCAATGAAAGCCCAAGA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
|||||
1157 TTGATCCAATCTAGAGCGCGCTCAAAATTTGCATATGGAACACAAACAT 1206
398 AspTyrPheAspHisTrpAspValValGlyTyrThrArgGluGlySerSe 414
|||||

```

```
1207 GATTATTTTACCACATCATATATATAATCGGATGCACACGTCAGGAATAATAC 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
1257 CACGCATCCCAATTCAGGACTTCGCACTATCATGTCGGATGGCCAGGG 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
1307 GAGAGAATGGATGTACGTAGGCAAAATAAACGACGTCAAGTTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
1357 GACATACTGGAATAAACACGAGACAGTTACGATCAATCAGATGGATG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
1407 GGCTAATTTTTCAGTAATGAGGATCTGTTCCATTTGGGTGAAACGA 1455
seq_name: /cgn2_6/ptodata/2/ina/6B_comb.seq:us-09-170-670-15

seq_documentation_block:
; Sequence 15, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
; US-09-170-670-15

alignment_scores:
Quality: 1860.50 Length: 483
Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

alignment_block:
US-09-590-375-1 x US-09-170-670-15 ..
Align seg 1/1 to: US-09-170-670-15 from: 1 to: 1455
1 AspGlyLeuAsnGlyThrMetGlnTyrTyrGluTrpHisLeuGluAs 17
7 AATGGGACAAATGGGACGATGATGAATCTTGAATGGCACTGCCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34
57 TGATGGGAATCACTGGAATAGATTAAAGATGATGCTAGTATCTAAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATACCGCTATTGTTGATTCGCCCTGCCCTGGAAAGGACTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspGlyGluPh 67
157 CAAAATGATGTGGGTGATGGACCTATGATCTTTATGATTTAGGGAAT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGGACACGCTAGTCAATTCG 256
```

```
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGTCGCCATCCATGCTTTAAAGAATAATGCGTTCACAGTTTATGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTAGTGATGAACCATAAAGGAGGAGCTGATGTACAGAAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134
357 TGTGCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
407 CAAATGAGGCTTGGACTAAGTTTATTTCCAGGGAGGGTAAATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
457 TCAGACTTTAAATGGCGTGGTATCATTTTCGATGGTGTAGATTGGGATCA 506
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 ATCACCACAAATCCAAATCGTATCTACAAATTCGAGGTGATGGTAAGG 556
182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197
557 CATGGGATTTGGGAAGTAGATTTCGAAAATGGAATATGATTATTTAATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspLulLeuLysAs 214
607 TATGCGAGATGATAGATGGATCATCCGAGGTAGTAAATGAGCTTAGAAG 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
657 ATGGGGAGAAATGATACAAATACATTAATCTTGATGGATTTAGGATCG 706
231 spAlaIleLysHisIleProPheTrpTrpTrpSerAspTrpValArgHis 247
707 ATGCGGTGAAGCATATTAAATATAGCTTTTACAGTGATTTGGTGACCAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
757 GTAAGAAACCAACGAGGGAAGAAATGTTGCTGCTGCTGAATTTTGAA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
807 AAATGATTTTAGTGCCTTGGAGAACTATTTAAATATAAACAACTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 ATCTGCTTTTGATGTCCTCCCTTCATTATATCTTTATACGCGTCAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
907 AGTGGAGGCAACTATGACATGGCAAAACTTCTTAATGSAACGGTTGTCA 956
314 uAlaHisProMethHisAlaValThrPheValAspAsnHisAspThrGlnp 331
957 AAAACATCCAAATGATGCGGTAACCTTTTGTGGATAATCAGGATCTCAAC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
1007 CTGGGGAATCATATTAGATCATTTTGTACAAAGATGTTTAAAGCCACTTGT 1056
348 TyrAlaThrIleLeuThrArgGlyGlyTyrProAsnValPheTyrG 364
1057 TATGCGCTTATTTTAAACAAGAGACACAGGCTATCCCTCTGCTCTTATGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
1107 TGACTACTATGGAATTCACACATAGTGTCCCGCAATGAAGCCAAGA 1156
```

```

381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||
1157 TTGATCCAATCTAGAGGCGCTCAAAATTTTGCATATGGAACACAACAT 1206

398 AspTyrPheAspHisTrpAspValValGlyTyrTrpArgGluGlySerSe 414
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1207 GATTATTTTGACCATCAATAATATCGATGACGACAGTGAAGGAATAC 1256

414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1257 CACGATCCCAATTCAGACTTGCACATATCATGTCGGATGGCCAGGG 1306

431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1307 GAGAGAAATGGATGTACGTAGGCGAAATAAAGCAGGTCAAGTTGGCAT 1356

448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1357 GACATAACTGGAAATAAACCCAGGAACAGTTACGATCAATGCAGATGGATG 1406

464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1407 GCCTAATTTTTCAGTAATGGAGATCTGTTCCATTTGGGTGAACGA 1455

```

seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:US-09-193-068-10

seq\_documentation\_block:

; Sequence 10, Application US/09193068

; Patent No. 6197565

; GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan

; APPLICANT: Kjuulff, S ren

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Andersen, Carsten

; TITLE OF INVENTION: Amylase Variants

; FILE REFERENCE: 5709.000-US

; CURRENT APPLICATION NUMBER: US/09/193.068

; CURRENT FILING DATE: 1998-11-16

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 1455

; TYPE: DNA

; ORGANISM: Bacillus sp.

; US-09-193-068-10

alignment\_scores:

Quality: 1860.50

Ratio: 4.327

Gaps: 2

Percent Similarity: 89.027

Percent Identity: 66.460

alignment\_block:

US-09-590-375-1 x US-09-193-068-10 ..

Align seg 1/1 to: US-09-193-068-10 from: 1 to: 1455

```

1 AspGlyLeuAsnGlyThrMetGlnTyrGlyThrGlnHisLeuGluAs 17
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
7 AATGGCAAAATGGGCGATGATGCAATACTTTGAATGGCATTCGCTAA 56

17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
57 TCATGGGATCACTGGAATAGATTAAGAGATGCTAGTAACTAAGAA 106

34 sPalAclylThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
107 ATAGAGTATAACCGCTATTTGGATTCCGCTGCGCTGGAAGGAGCTCG 156

51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspGlyGluPh 67
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
157 CAAATGATGTGGGGTATGGAGCCATGATCTTTATGATTTAGGGGAATT 206

```

```

67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
207 TAATCAAAAGGGGCGGTTCTGCTACCTAAAGTATGGACACGCTAGTCAATTGS 256

84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
257 AGTCTGCCATCATGCTTTAAAGAAATAATGGCGTTCAAGTTTATGGGAT 306

101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
307 GTAGTGATGAACCATAAAGGAGAGCTGATGCTACAGAAACGCTTTTTCG 356

117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
357 TGTGAGGTGAATCCAATAACCGGAATCAAGAAATATCTGGGGACTACA 406

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
407 CAATTGAGGCTTGGACTAAGTTTGTATTTTCCAGGGAGGGGTAATACATAC 456

151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
457 TCAGACTTTAAATGGCGTTGGTATCATTTCCGATGGTGTAGATTGGGATCA 506

167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
507 ATCAGCACAATTCCAAAATCGTATCTACAAATTCGAGGTGATGGTAAGS 556

182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
557 CATGGGATTGGGAAGTAGATTCCGAAATCGAAATTTATGATTATTTAATG 606

198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
607 TATGCAGATGTAGATATGATCATCCGAGGAGTAGTAATGAGCTTGAAG 656

214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
657 ATGGGAGAAATGCTATACAAATACATATAAATCTTGATGGATTAGGATCG 706

231 sPalAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
707 ATGCGGTGAAGCATATTAATATAGCTTTTACAGCTGATTGGTTGACCCAT 756

248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGlyTyrTrpLy 264
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
757 GTAAGAACCCACACGGGAAAGAAATGTTTGTGTTGCTGAATTTGGAA 806

264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
807 AAATGATTTAGTGCTTGGAGAACTATTTAAATAAAACAAACACTGGAATC 856

281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
857 ATTCTGCTTTGATGTCCCTTCATTATAATCTTTATAACGCGTCAAT 906

298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
907 AGTGGAGGCAACTATGACATGGCAAACTCTTTAATGGAACGGTGTGTTCA 956

314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
957 AAAGCATCAATGCTGCGCTAACTTTTGTGGATAATCAGATTCTCAAC 1006

331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1007 CTGGGGAATCATTAGAAATCATTTGTACAAGATGGTTTAAAGCCACTTGT 1056

348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrG 364
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1057 TATGCCCTTATTTTAAAGAGAACAGGCTATCCCTCTGCTCTCTATGG 1106

364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381

```

```

|||||
1107 TGACTACTATGGAAATTCACACATAGTCCAGCAATGAAAGCCCAAGA 1156
|||||
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
|||||
1157 TTGATCCATCTTTAGAGCGCGCAAAATTTTGCATATGGAACAACAT 1206
|||||
398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
|||||
1207 GATTATTTTGACCATCATATATATATCGGATGGACAGCTGAAGGAATAC 1256
|||||
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
|||||
1257 CAGCGCATCCCAATTCAGGACTTCGCACTATCATGTCCGATGGCCAGGG 1306
|||||
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
|||||
1307 GAGAGAAATGGATGTACGTAGGCAAAATAAAGCAGGTCAAGTTGGCAT 1356
|||||
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
|||||
1357 GACATAACTGGAATAAACCCAGGAACAGTTACGATCAATGCAGATGGATG 1406
|||||
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
1407 GGCTAATTTTCAGTAATGAGGATCTGTTCCATTGGGTGAAACGA 1455
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-193-068-14

```

## seq\_documentation\_block:

```

; Sequence 14, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjrulff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Anyase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-193-068-14

```

## alignment\_scores:

```

Quality: 1860.50      Length: 483
Ratio: 4.327          Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

```

## alignment\_block:

```
US-09-590-375-1 x US-09-193-068-14 ..
```

```
Align seg 1/1 to: US-09-193-068-14 from: 1 to: 1455
```

```

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
7 AATGGGCAAAATGGGAGGATGATGCAATCTTTGAATGGCACTGGCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA 34
57 TGATGGGAATCACTGGAATAGATAGAGATGATGCTAGTAATCTAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATAACCGCTATTTGGATTCCGCTGCCCTGGAAGGACCTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67

```

```

|||
157 CAAAATGATGGGTATGGAGCTATGATCTTTATGATTAGGGAATT 206
|||
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
|||
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACAGTAGTCAATGG 256
|||
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
|||
257 AGTCTGCCATCCATGCTTTAAAGAATAAATGGCGTTCAAGTTTATGGGAT 306
|||
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
|||
307 GTAGTGATGAACCATAAAGGAGGAGCTGATCTACAGAAAACGTTCTTGC 356
|||
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
|||
357 TGTGAGGTGAATCCCAATACCGGAATCAAGAAATATCTGGGACTACA 406
|||
134 hrIleAspAlaIleThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
|||
407 CAATTGAGGCTTGGACTAAGTTTGATTTTCCAGGAGGGGTAAATACATAC 456
|||
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
|||
457 TCAGACTTTAAATGGCGTGTGATCATTTGATGTTGATGTTAGATTGGGATCA 506
|||
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 181
|||
507 ATCAGGACAATCCAAATCGTATCTACAAATTCGAGGTGATGGTAAGG 556
|||
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
|||
557 CATGGGATTGGGAAGTAGATTCGGAAATGGAATATGATTATTATTAATG 606
|||
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
|||
607 TATGCGAGATGATAGTATGATCATCCGAGGAGTAGTAAATGAGCTTAGAAG 656
|||
214 pTyrGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
|||
657 ATGGGAGAAATGGTATACAAATACATTAAATCTTGATGATTTAGGATCG 706
|||
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
|||
707 ATCGGTGAAGCATATTAATATAGCTTTACACGTGATTTGTTGACCCAT 756
|||
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
|||
757 GTAAGAAACCAACGGGAAAGAAATGTTTGTGCTGCTGAATTTTGGA 806
|||
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
|||
807 AATGATTTAGGTGCTTGGAGAACTATTAAATAAACAACACTGGGAATC 856
|||
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
|||
857 ATTCTGTCTTTGATGTCCTCCCTTCATTATAATCTTTATAACGGCTCAAT 906
|||
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl 314
|||
907 AGTGGAGGCAACTATGACATGGCAAACTTCTTAATGGAACGGTTGTTC 956
|||
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
|||
957 AAGCATCCCAATGCAUGCCGTACTTTTGGGATAATACAGATTCTCAAC 1006
|||
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
|||
1007 CTGGGAATCATTTAGAAATCATTTGTACAAGAATGGTTTAAAGCCACTTGT 1056
|||
348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrGl 364
|||

```



```

1057 TATGCGCTTATTTTAAAGAGAACAAAGCGGTATCCCTCTGCTCTTATGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1107 TCACCTACTATGAATTCACACACATAGTGTCCACCAATGAAGCCACA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1157 TTGATCCCAATCTAGAGCGGCTCAAAATTTTGCATATGAACACAACAT 1206
398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1207 GATTTTTTGGACCAATAATATATATCGGACACGTGAAGAAATAC 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1257 CAGCATCCCAATTCAGACITTCGACATATCATGTCGGATGGCCAGGG 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1307 CAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1357 GACATACTGGAATAAACACAGGACAGTTAGATCAATGATGGATGGATG 1406
464 pGlyGluPheThrAsnGlyGlySerValSerValTyrValAsnGln 480
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
1407 GCGTAATTTTCAGTAATGAGGATCTGTTCCATTTGGGTGAACGA 1455
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-10
seq_documentation_block:
; Sequence 10, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183.412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-183-412-10

```

```

alignment_scores:
  Quality: 1860.50      Length: 483
  Ratio: 4.327          Gaps: 2
  Percent Similarity: 89.027  Percent Identity: 66.460

```

```

alignment_block:
US-09-590-375-1 x US-09-183-412-10 ..
Align seg 1/1 to: US-09-183-412-10 from: 1 to: 1455

```

```

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
7 AATGGACAAATCGGACGATGATGCAATACTTTGAATGGCACTTGCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
57 TCATGGGAATCACTGGAATAGATTAAAGAGATGATGCTAGTAATCTAAGAA 106
34 sAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
107 ATAGAGGTATAACCGCTATTTCGATTCGCCCTGCCCTGGAAAGGACTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
157 CAAATGATGTCGGGTATCGAGCTATGATCTTTATGATTTAGGGCAATT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
207 TAATCAAAAGGGGACGGTTCCGTACTAAAGTATGGACACGTAGTCAATTGG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
257 AGTCTGCCATCCATCGCTTTAAAGAATAATGGCGTTCAAGTTTATGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
307 GTAGTGATGAACCAATAAAGGAGGAGTGATGCTACAGAAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
357 TGTGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
407 CAATTGAGCTTGGACTAAGTTTGAATTTCCAGGGAGGGGTAACTACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
457 TCAGACTTTAAATGCGTGTGGTATCATCTTCGATGGTGTAGATTGGGATCA 506
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
507 ATCAGACAAATTCACAAATCGTATCTACAAATTCGAGGTGATGGTAAGG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
557 CATGGATTGGGAAGTAGATTTCGGAATAATGGAATATGATATTATTATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
607 TATGCAGATGTAGATATGATCGGAGGTAGTAAATGAGCTTAGAAG 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
657 ATGGGGAATGATACAAATACATTAATCTTGAATGATTTAGGATCG 706
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
707 ATGCGGTGAAGCATATTAAATATAGCTTTACACGTGATTTGGTTGACCCAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
757 GTAAGAACGCAACGGGAAAAGAAATGTTTGTGCTGAATTTTGGAA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
807 AAATGATTTAGGTGCTTGGAGAACTATTATAATAAACAACAACTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
857 ATTCTGCTTTCATGTCCTTCATTAATACTTTTATAACGCGTCAAAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314

```



```

: ZIP: 10174-6401
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/354,191A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/600,656
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Lambiris, Elias J.
: REGISTRATION NUMBER: 33,728
: REFERENCE/DOCKET NUMBER: 4318.204-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 867 0123
: TELEFAX: 212 867 0298
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1455 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-354-191A-5

alignment_scores:
    Quality: 1860.50      Length: 483
    Ratio: 4.327          Gaps: 2
    Percent Similarity: 89.027    Percent Identity: 66.460

alignment_block:
US-09-590-375-1 x US-09-354-191A-5 ..

Align seg 1/1 to: US-09-354-191A-5 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
: ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
7 AATGGGACAAATGGGACGATGATGCATCTCTTGAATGGCATTGCCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34
: ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
57 TGATGGGATCACTGGANATAGATTAGAGATGATGCTAGTAACTAAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
: ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
107 ATAGAGGTATACCCGCTATTGTGGATCCGCTGCTGGAAGGGACTTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
: ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 CAAATATGATGTGGGGTATGGAGCTATGATCTTTATGATTTAGGGGAAT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGCTAGTCAATTCG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
: || ||||| ::::: ||||| ::::: ||||| ::::: |||||
257 AGTCTGCCATCCATGCTTTTAAAGAAATAATGGCGTTCAAGTTTATGGGCAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
307 GTAGTGATGAACCATAAAGAGAGAGCTGATGCTACAGAAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
357 TGTGCGAGGTGAATCCAAATTAACCGGAATCAAGAAATATCTGGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyValArgAsnAsnAlaTyr 150

```

seq\_documentation\_block:

; Patent No. 6297038

APPLICANT: Bisgard-Frantzen, Henrik

APPLICANT: Borchert, Torben Vedel

; NUMBER OF SEQUENCES: 32

ADDRESSEE: No. 62970380 No. 62970

CITY: New York

STATE: New York





```
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1455 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-861-837-4

alignment_scores:
  Quality: 1835.50      Length: 483
  Ratio: 4.319          Gaps: 2
  Percent Similarity: 87.992  Percent Identity: 66.253

alignment block:
US-09-590-375-1 x US-08-861-837-4 ..

Align seg 1/1 to: US-08-861-837-4 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
7 AATGGAACAATGGTACTATGATGCAATATTCGAATGGTATTGGCAAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
57 TGACGGGAATCATGGACAGGTTGAGGGAGTACGAGCTAACTTAAAGA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
107 GTAAAGGATAACAGCTGTATGATCCACCTGCATGTAAGGGGACTTCC 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGlu 67
157 CAGAATGATGTAGTGTATGAGCCTATGATTTATATGATCTTGGAGATT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeu 84
207 TAACCAAGAGGGGACGTTCTGACAAATATGGAACACGCAACGCTAC 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGGCTGCGGTGACCTCTTTAAAAAATACGCGCATTCAGGTATATGGTAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTCGTCATGAATCATAAAGTGGAGCAGATGGTACGGAATTTGTAATGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 GGTAGAAGTGAATCGGAGCAACCGAAACACGAGAAACCTCAGGAGATG 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
407 CAATAGAGCGGTGACAAAGTTTTCATTTCTGGAAGAGGAATAACCAT 456
151 SerAspPheLysTyrArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
457 TCCAGCTTTAAGTGGCGTGTATCATTTTTCATGGGACAGATTGGGATCA 506
167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 GTCACGCCAGCTTCAAAACAAAATATATAAATTCAGGGGAACAGGCAAG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
557 CTTGGAGCTGGGAAGCTCATACAGAAATGGCAACTATGACTACTTCTTAIG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGACGTGGATATGATGATCACCACCAAGTAATACATGAATAGAAA 656

seq_name: /cqn2_6/ptodata/2/ina/6A_COMB.seq:US-08-600-656-4
seq documentation block:
; Sequence 4, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
```



```

414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
1257 CCCCCCAATTCAGGCTCCCAACCAATATGTCAGATGGTCCAGGT 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
1307 GTAACAAATGGATGTATGGGGGAAAAATAAACGGGACAAAGTTTGAGA 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
1357 GATATTACCGGAAATAGGACAGGCACCGTCACAATTAATGCACAGCGATG 1406
464 pGlyGluPhePheThrAsnGlySerValSerValTyrValAsnGln 480
1407 GGTAAATTCCTCTCTAATGGAGGTCCTGTTCCGTTGGGTGAAGCAA 1455
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-9

```

```

seq_documentation_block:
; Sequence 9, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; EARLIER FILING DATE: 1998-10-13
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-170-670-9

```

```

alignment_scores:
Quality: 1835.50      Length: 483
Ratio: 4.319          Gaps: 2
Percent Similarity: 87.992 Percent Identity: 66.253

```

```
alignment_block:
```

```
US-09-590-375-1 x US-09-170-670-9
```

```
Align seg 1/1 to: US-09-170-670-9 from: 1 to: 1455
```

```

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
7 AATGGAACAAATGGTACTATGATGCAATATTCGAATGGTATTGGCAA 56
17 naspGlyGlnHisTrpAsnArgLeuHisaspAlaAlaLeuSerA 34
57 TGACGGGAATCATFTGGAACAGGTTGAGGATGACGACGCTAACTTAAAGA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
107 GTAAAGGGATAACAGCTGTATGATGCCACCTGCATGGGAAGGGACTTCC 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAGAAATGATGTAGTTATGGAGCCTATGATTTATATGATCTTGGAGATT 206
67 easnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAACCAAGAGGGGACGGTTCGTACAAAATATGGAACACGCAACAGCTAC 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100

```

```

257 AGCGCTCGGTGACCTCTTTAAAAAATAACGGCATTCAGGTATATGTGTAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTGCTCATGATCATAAAGGTGGAGCAGATGGTACCGAAATTTGTAATGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134
357 GGTAGAAGTGAATCGGGACCAACCGAAACAGGAAACCTCAGGAGAGTATG 406
134 hrtIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
407 CAATAGAAGCGTGGCAAAAGTTTGAATTTCTCTGGAAGAGGAAATAACCAT 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
457 TCCAGCTTTAAGTGGCGCTGGTATCATTTTGTGGACAGATTTGGGATCA 506
167 n...ArgTyrGlnGlnAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 GTCACGCCAGCTTCAAAACAAATAATATAAATTCAGGGGAACAGCAAGG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTrpLeuLeu 197
557 CCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTATCTTATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGACGTGGATATGATCACCAGAGTAATACATGAACCTAGAAA 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
657 CTGGGAGTGTGTATACGAATACACTGAACCTTGATGATTTAGAATAG 706
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATGCACTGAACATATAAATATATAGCTTTACGAGAGATTTGGCTTACACAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrp 264
757 GTGCGTAACACCACAGGTAAACCAATGTTTGCAGTGGCTGAGTTTGGAA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
807 AATGACCTTGGTGCATTAATAAACTATTGTAATAAAACAAGTTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 ACTCGGTGTTGATGTTCTCTCCACTATAAATTTGACAAATGCATCTAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
907 AGCGGTGGTTATTATGATATGAGAAATATTTAAATGGTCTGTGTGTGCA 956
314 uAlaHisPromethHisAlaValThrPheValAspAsnHisAspThrGlnP 331
957 AAAACATCCACACACATGCCGTTACTTTTGTGATAAACCATGATTCTCAGC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
1007 CCGGGGAAGCATTTGGAATCCTTTGTTCAACAATGTTTAAACCCACTTGCA 1056
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrG 364
1057 TATGCATTTGTTCTGACAAAGGGAACAAGGTATCTCTCCGTATTTTATGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
1107 GGATTTACTACGTATCCCAACCCATGCTGCTCCGGCTATGAAATCTAAAA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397

```



1157 TAGACCCCTCTTCGACGACGCTCAAACTTTTGGCTATGTCAGCAGCAT 1206  
 398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414  
 1207 GATTAATTTGATCATCATGATATATATCGGTTGGACAAGAGGAAATAG 1256  
 414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431  
 1257 CTCCCATCAAATTCAGGCCCTTGCCACCATATATGTCAGATGTCAGGTG 1306  
 431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyClnThrTrpThr 447  
 1307 GTAAACAATGATGATGATGTTGGGAAAAATAAAGCGGGCAAGTTGGAGA 1356  
 448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464  
 1357 GATATTACCGGAATAGACAGGACCGCTCACAAATTAATGACAGCGATG 1406  
 464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480  
 1407 GGGTAATTTCTCTGTTAATGAGGCTCGCTTTCGGTTTGGGTGAAGCAA 1455  
 seq\_name: /cgn2\_6/ptodata/2/ina/68\_COMB.seq:us-09-170-670-14

seq\_documentation\_block:  
 ; Sequence 14, Application US/09170670  
 ; Patent No. 6187576

GENERAL INFORMATION:  
 ; APPLICANT: Svendsen, Allan  
 ; APPLICANT: Borchert, Torben  
 ; APPLICANT: Bisgaard-Frantzen Henrik  
 ; TITLE OF INVENTION: Alpha-Amylase Mutants  
 ; FILE REFERENCE: 5276.200-US  
 ; CURRENT APPLICATION NUMBER: US/09/170,670  
 ; CURRENT FILING DATE: 1998-10-13  
 ; EARLIER APPLICATION NUMBER: 1172/97  
 ; EARLIER FILING DATE: 1997-10-13  
 ; EARLIER APPLICATION NUMBER: 60/063,306  
 ; EARLIER FILING DATE: 1997-10-28  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 14  
 ; LENGTH: 1455  
 ; TYPE: DNA  
 ; ORGANISM: Bacillus sp.  
 US-09-170-670-14

alignment\_scores:  
 Quality: 1835.50 Length: 483  
 Ratio: 4.319 Gaps: 2  
 Percent Similarity: 87.992 Percent Identity: 66.253

alignment\_block:

US-09-590-375-1 x US-09-170-670-14 ..

Align seg 1/1 to: US-09-170-670-14 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTrpGluTrpHisLeuGluAs 17  
 7 AATGGAACAAATGCTGATGATGATGATGATGATGATGATGATGATGATG 56  
 17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34  
 57 TGACGGGAATCATTTGGAACAGGTTGAGGAGTGCACCATTAACITTAAGA 106  
 34 spAlaGlyIleThrAlaIleThrProAlaTyrLysGlyAsnSer 50  
 107 GTAAAGGGATAACACCTCTATGATGCCACCTGCATGGAAGGGGACTTCC 156  
 51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyLuph 67  
 157 CAGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 206

67 easnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84  
 207 TAACCAAGAAGGGGACCGTTTCGTACAAAATATGGAACACGCAACCACTAC 256  
 84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100  
 257 AGGTCGCGTACCTCTTTAAAAAATAACGCGCATTCAGGTATATGGTGT 306  
 101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117  
 307 GTCGTCATGAATCATATAAGGTGGAGCAGATGTCGGAATTTGTAATGTC 356  
 117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134  
 357 GGTAGAAGTGAATCGGACCAACCGAACCAGGAACCTCAGGAGAGATG 406  
 134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150  
 407 CAATAGAAGCGTGGACAAGTTGATTTCTCTGGAAGAGGAATAACCAT 456  
 151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167  
 457 TCCAGCTTTAAGTGGCTGGTGTATCATTTTGTATGGACAGATTTGGATCA 506  
 167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181  
 507 GTCAGCCGACGCTTCAAAACAAAATATATAATTCAGGGGAACAGCAAGG 556  
 182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197  
 557 CTGGGACTGGGAATCGATACAGAGAATGGCAACTATGACTATCTTATG 606  
 198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214  
 607 TATGACAGCTGGATATGGATCACCCAGAAGTAATACATGAACCTTAGAAA 656  
 214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231  
 657 CTGGGAGTGGTATACGAATACACTGAACCTTCATGATTTAGCAATAG 706  
 231 spAlaIleLysHisIleProPheTrpTyrTrpSerAspTrpValArgHis 247  
 707 ATGCAGTGAACATATATAAATATAGCTTTACGAGAGATTTGGCTTACAC 756  
 248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264  
 757 GTGCGTAACACACACAGGTAAACCAATGTTTGCAGTGGCTGAGTTTGGAA 806  
 264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281  
 807 AATGACCTTGGTGAATTTGAAACTATTTGAATAAACAAGTTGGAATC 856  
 281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297  
 857 ACTCGGTGTTGATCTCTCCACTATATTTGTCAACAATGTTTAAACCACT 906  
 298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl 314  
 907 AGCGGTGTTTATGATGATGAGAAATATTTTAAATGTTTCTGTGGTGCA 956  
 314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331  
 957 AAAACATCCAACACATGCGGTACTTTTGTGATCAACCATGATTTCTCAG 1006  
 331 roGlyLysSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347  
 1007 CCGGGAAGCATTTGGAATCTCTTGTTCACAATGTTTAAACCACTTGCA 1056  
 348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrGl 364  
 1057 TATGATGTTGTTCTGACAAGGGAACAGGTTTATCTCGTATTTTATGG 1106

364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381  
|||||  
1107 GGATTACTACGGTATCCCAACCCCATGGTGTCCGGCTATGAAATCTAAAA 1156  
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397  
|||||  
1157 TAGACCCCTCTTCTCGAGGCACGCTCAAACTTTGCCATATGGTACGACAT 1206  
398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerse 414  
|||||  
1207 GATTACTTTGATCATCATGATATTATCGGTTGGACAAGAGAGGGAATAG 1256  
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431  
|||||  
1257 CTCCCATCCAAATTCAGGCCCTTGCCACCATTATGTCAGATGGTCCAGGTG 1306  
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447  
|||||  
1307 GTAACAATGGATGTATGTGGGAAAATAAAGCGGACAAAGTTTGAGA 1356  
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464  
|||||  
1357 GATATTACCGGAAATAGACAGGCACCGTCACAATTAATGCAGACGGATG 1406  
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480  
|||||  
1407 GGGTAATTCTCTGTTAATGGAGGGTCCGTTTCGGTTTGGGTGAAGCAA 1455

OM of: US-09-590-375-1 to: N\_Geneseq\_1101:\* out\_format : pfs

Date: Nov 28, 2001 6:32 PM

About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

```
-MODE=frame-p2n.model -DEV=xlhb
-Q/cn2_1/USPO.spool/US9590375/runat_28112001_152038_21086/app_query.fasta_1.1092
-DB=N_Geneseg_1101 -QFMT=fastap -SUFFIX=ing -GAPOP=12.000
-GAPMAP=4.500 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-XGAPOP=4.500 -CGAPEAT=0.050 -XGAPOP=10.000 -XGAPEAT=0.500
-FCGAP=6.000 -FGAPEAT=7.000 -YGAPOP=10.000 -YGAPEAT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfis
-NORM-ext -MINLEN=0 -MAXLEN=2000000000
-USER=US9590375_@CGN_1_1_386 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
```

## Search information block:

```

Query: US-09-590-375-1
Query length: 480
Database: N_Geneseq_1101:*
Database sequences: 930621
Database length: 428662619
Search time (sec): 174.840000

```

**score\_list:**

[illegible]

```
/SID52/gcgdata/geneseq/NA1998.DAT :AAV09764 + 1723..50 2889..35 7.3e-
/SID52/gcgdata/geneseq/NA1999.DAT :AAX84394 + 1723..50 2889..35 7.3e-
/SID52/gcgdata/geneseq/NA1999.DAT :AAX82650 + 1723..50 2889..35 7.3e-
/SID52/gcgdata/geneseq/NA1999.DAT :AAX21818 + 1723..50 2889..35 7.3e-
/SID52/gcgdata/geneseq/NA1999.DAT :AAV08975 + 1723..50 2889..35 7.3e-
seq_name: /SID52/gcgdata/geneseq/NA2000.DAT :AAA70314
```

seq\_name: /SIDS2/gcgcdata/geneseq/geneseq/NA2000.DAT:AAA70314

## seq documentation block:

seq\_documentation\_block.  
ID AAA70314 standard; DNA; 1745 BP.

AA  
AC AAA70314:

DT 19-DEC-2000 (first entry)

DE Bacillus sp. liquefying alpha-amylase #2 coding sequence

XX Liquefying alpha-amylase; detergent; starch industry; brewing industry;  
KW pharmaceutical industry; food industry; fibre industry; ds.  
KW

OS Bacillus sp.

Key	Location/Qualifiers
-----	---------------------

FT	key	location/s
FT	CDS	190..1695

```
product= "alpha-amylase"
```

AA  
PN  
EP1022334-A2.

XX  
PD  
26-III-2000XX  
PF 20-DEC-1999. 99EP-0125399

XX  
DB 21-DEC-1000.  
09 TD-0353487

PR 21-DEC-1998; 98JP-0362488.  
VY

PA (KAOS ) KAO CORP.

PI Nagihara H, Kitayama Y

DR WPI; 2000-516014/47.

XX

PT comprises a residual

XX

XX

CC Bacillus sp. The inv

CC KSM-K36 and KSM-K38,

CC resistant and thus a

cc detergents.

SQ Sequence 1745 BP; 50

Quality: 2687

Percent Similarity: 100.

alignment block:

03-03-330-313-I X AAA/US

Align seg 1/1 to: AAAA/0

I AspGlyLeuAsnGlyI

```

253 GATGATTCAACGGTACGATGATGAGTATTTATGATGGCATTTGGAAAA 302
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
|||||
303 CGACGGGAGCATTCGAATCGGTTCCACGATGATGCCGACGTTTGGTG 352
34 sAlaGlyIleThrAlaIleProIleProAlaIleLysGlyAsnSer 50
|||||
353 ATGCTGGTATTACAGCTATTGGATTCGCCAGGCTACAAAGGTAATAGT 402
51 GlnAlaAspValGlyTyrGlyAlaIleAspLeuValGlyGluPh 67
|||||
403 CAGCGGATTTGGGTGCGTACGATCCTTTATGATTTAGGAGATT 452
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
|||||
453 CAATCAAAAGGGTACTGTGTGAAGAAATACGGAATTAAGCACAGCTTG 502
84 luAtqAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
|||||
503 AACGAGCTATTGGGTCCCTTAATCTAATGATCAATGTATACGGAGAT 552
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
|||||
553 CTCGTGATGAATCATAAATGGGAGCTGATTTTACGGAGGCGAGTGAAGC 602
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
|||||
603 TGTTCAGTAATCAACGAATCCTTGGCAGGATATTTTCAGGTGCCTACA 652
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
|||||
653 CGATTGATCGTGCAGCGGTTTCACATTTTCAGGCGGTACACAGCCGAT 702
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGI 167
|||||
703 TCAGATTTTAAGTGGAGATGTTCCATTTTAATGGTCTGACTGGGATCA 752
167 nArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsnTrpAsnT 184
|||||
753 GCGCTATCAGAAATCATATTTTCCGCTTTGCCAATACCAACTGGAACT 802
184 rpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsn 200
|||||
803 GCGGATGGATGAAGAGAACGGTAATATGATACCTGTTAGGATCGAAT 852
201 IleAspPheSerHisProGluValGlnAspGluLeuLysAspTrpGlySe 217
|||||
853 ATCGACTTTAGTCATCCAGAGTACAGATGAGTTGAAGGATTTGGGATG 902
217 rTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaIleL 234
|||||
903 CTGCTTTACGATGAGTATGATTTGGATGTTATCGTTTACATGCTATTA 952
234 ysHisIleProPheTrpTyrThrSerAspTrpValArgHisGlnArgAsn 250
|||||
953 AACATATTCATCTCTGTATACATCTGATGGGTTTCGGCATCAGCGCAAC 1002
251 GluAlaAspGlnAspLeuPheValGlyGluTyrTrpLysAspAspVa 267
|||||
1003 GAAGCATCAAGATTTATTTGCGTAGGGAATATTGGAAGGATGACGT 1052
267 lGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluMetSerLeup 284
|||||
1053 AGGTGCTCTCGAATTTTATTAGATCAATGAATTTGGAGATGCTCTAT 1102
284 heAspValProLeuAsnTyrAsnPheTyrArgAlaSerGlnGlnGlyGly 300
|||||
1103 TCGATGTTCCACTTAATATAATTTTTTACGGGCTTCACAACAAGGTGGA 1152
301 SerTyrAspMetArgAsnIleLeuArgGlySerLeuValGluAlaHispr 317
|||||
1153 AGCTATGATATCGTAATATTTTACGAGGATCTTTAGTAGAAGCCGATCC 1202

```

```

317 oMetHisAlaValThrPheValAspAsnHisAspThrGlnProGlyGluS 334
|||||
1203 GATGCATGCGATTACGTTTGTGTAATCATGATACTACGCCAGGGGAGT 1252
334 erLeuGluSerTrpValAlaAspTrpPheLysProLeuAlaIleAlaThr 350
|||||
1253 CATTAGAGTCATGGTTGCTGATTGGTTTAAAGCCACTTGTCTATGCGACA 1302
351 IleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGlyAspTyrTy 367
|||||
1303 ATTTTGACGCGTGAAGGTGTTTATCCAAATGTATTTTACGGTGATTACTA 1352
367 rGlyIleProAsnAspAsnIleSerAlaLysLysAspMetIleAspGluL 384
|||||
1353 TGGGATTCCTAAGCATACATTTTCAGTAAAAAGATATGATGATGAGC 1402
384 euLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHisAspTyrPhe 400
|||||
1403 TGCTTGATGCACGTCAAAATTTACGCATATGGCACGCGCATGACTATTTT 1452
401 AspHisTrpAspValValGlyTyrTrpArgGluGlySerSerSerArgpr 417
|||||
1453 GATCATTTGGATGTTGTAGGATGGACTAGGGAAGGATCTCTCTCCAGACC 1502
417 oAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyGlySerLysT 434
|||||
1503 TAATTCAGGCTTGGCAGCTATTATGTGCAATGCACCTGGTGGTTCCAAGT 1552
434 rpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThrAspLeuThr 450
|||||
1553 GGATGTATGTAGGACGTCAGAAATGCAGGACAAACATGACAGATTTAACT 1602
451 GlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTrpGlyGluPh 467
|||||
1603 GGTAAATACGGAGCGTCCGTTACAAATTAATGCGGATGGATGGGCGGAAT 1652
467 ePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
|||||
1653 CTTTACGAATGGAGGATCTGTATCCGTGACGTGAACCA 1692

seq_name: /SIDS2/5cgcdata/geneseq/geneseq/NA2000.DAT:AAA70313
seq_documentation_block:
ID AAA70313 standard; DNA; 1650 BP.
XX
AC AAA70313;
XX
DT 19-DEC-2000 (first entry)
XX
DE Bacillus sp. liquefying alpha-amylase #1 coding sequence.
XX
KW Liquefying alpha-amylase; detergent; starch industry; brewing industry;
pharmaceutical industry; food industry; fibre industry; ds.
XX
OS Bacillus sp.
XX
FH Key Location/Qualifiers
CDS 65..1570
FT /*tag= a
FT /product= "alpha-amylase"
XX
PN EPI022334-A2.
XX
PD 26-JUL-2000.
XX
PF 20-DEC-1999; 99EP-0125399.
XX
PR 21-DEC-1998; 98JP-0362487.
XX
PA 21-DEC-1998; 98JP-0362488.
XX
(KAOS ) KAO CORP.
XX

```

PI Hagihara H, Kitayama K, Hayashi Y, Igarashi K, Endo K, Ozaki K;  
 XX WPI: 2000-516014/47.  
 DR P-PSDB; AAB14821.  
 DR

XX New liquefying alkaline amylase, useful in a detergent composition  
 PT comprises a residual activity of not less than 70 % when treated under  
 PT specific conditions -  
 PT

XX Claim 6; Page 20-23; 34pp; English.

XX The present sequence is the coding sequence of a novel alpha-amylase from  
 CC Bacillus sp. The invention concerns the isolation of two new liquefying  
 CC alpha-amylases (and their coding sequences) from Bacillus sp. strains  
 CC KSM-K36 and KSM-K38, designated K36 and K38, of which this sequence  
 CC encodes one. The alpha-amylases of the invention are chelating-agent  
 CC resistant and thus are useful in the starch, brewing, fibre,  
 CC pharmaceutical and food industries, and especially as components of  
 CC detergents.  
 XX

SQ Sequence 1650 BP; 475 A; 267 C; 420 G; 488 T; 0 other;

# alignment\_scores:

Quality: 2618.00 Length: 480  
 Ratio: 5.477 Gaps: 0  
 Percent Similarity: 99.583 Percent Identity: 96.458

# alignment\_block:

US-09-590-375-1 x AAA70313 ..

Align seg 1/1 to: AAA70313 from: 1 to: 1650

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17  
 |||||  
 128 GATGCTTGAATGGAACCATGATGAGTATTTATGATGGCATCTAGACAA 177  
 |||||  
 17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSera 34  
 |||||  
 178 TGATGGGCACACTGGATCGTTCGATGATGATGCCGAGCTTAAATA 227  
 |||||  
 34 sPalaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50  
 ::|||  
 228 ATGCGGGTATTACAGCTATTGATACCCAGCCCTACAAAGGAAATAGT 277  
 |||||  
 51 GlnAlaAspValGlyTyrGlyAlaTrpAspLeuTyrAspLeuGlyGluPh 67  
 |||||  
 278 CAGGCTGATTTGGGTATGGTGCATACGACCTTTATGATTTAGGGGAGTT 327  
 |||||  
 67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84  
 |||||  
 328 TAATCAAAAAGGTACCGTTTCGAACCAATACGGACAAAGGCTCAGCTTG 377  
 |||||  
 84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100  
 |||||  
 378 AGCGAGCTATAGGGTCCCTAAAGTCGAATGATATCAATGTTTATGGGAT 427  
 |||||  
 101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117  
 |||||  
 428 GTCCGTAATGAATCAAAATTAGGAGCTGATTTACGGAGGCGATGCAAGC 477  
 |||||  
 117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134  
 |||||  
 478 TGTTCAAGTAATCTTCGAACCGTTGGCAGGATATTTTCAGGTGCTACA 527  
 |||||  
 134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150  
 |||||  
 528 CGATTGATGCATGGACGGGATTTGATTTCCAGGCGCAACAATGCCTAT 577  
 |||||  
 151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167  
 |||||  
 578 TCCGATTTTAAATGGAGATGGTTCCATTTTAAATGGCGTTAGTGGGATCA 627

167 nArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsnTrpAsnT 184  
 |||||  
 628 AGGCTATCAAGAAACCATCTTTTCGCTTTGCAATACGAACCTGGAAC 677  
 |||||  
 184 rpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsn 200  
 |||||  
 678 GCGGAGTGGATCAAGAGAATGTAATATGACTATTTATTAGGATCGAAC 727  
 |||||  
 201 IleAspPheSerHisProGluValGlnAspGluLeuLysAspTrpGlySe 217  
 |||||  
 728 ATGTACTTTAGCCACCCAGAGGTTCAAGAGGATTAAGGATTTGGGGAG 777  
 |||||  
 217 rTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaIle 234  
 |||||  
 778 CTGGTTTACGGATGAGTAGATTTAGATGGGTATCGATGGATGCTATTA 827  
 |||||  
 234 ySHisIleProPheTrpTyrThrSerAspTrpValArgHisGlnArgAsn 250  
 |||||  
 828 AGCATATTCCATTCTGGTATACGTGAGATTGGTTAGGCATCAGCGAAGT 877  
 |||||  
 251 GluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLysAspVal 267  
 |||||  
 878 GAAGCAGACCAAGATTTATTTCTGTAGGGGAGTATTTGAAGGATGACGT 927  
 |||||  
 267 lGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluMetSerLeup 284  
 |||||  
 928 AGGTGCTCTCGAATTTTATTAGATGAATGAATTGGGAGATGCTCTAT 977  
 |||||  
 284 heAspValProLeuAsnTyrAsnPheTyrArgAlaSerGlnGlnGly 300  
 |||||  
 978 TCGATGTTCCGCTCAATATAATTTTACGGGCTTCAAAGCAAGCGGA 1027  
 |||||  
 301 SerTyrAspMetArgAsnIleLeuArgGlySerLeuValGluAlaHisPr 317  
 |||||  
 1028 AGCTATGATATCGGTAATATTTTACAGGATCTTTAGTAGAAGCATCC 1077  
 |||||  
 317 oMethHisAlaValThrPheValAspAsnHisAspThrGlnProGlyGlu 334  
 |||||  
 1078 GATTCATGAGTTACGTTTGTGTAATCATGATCTACTCAGCCAGGAGAT 1127  
 |||||  
 334 erLeuGluSerTrpValAlaAspTrpPheLysProLeuAlaTyrAlaThr 350  
 |||||  
 1128 CATTAGAATCATGGGTGCTGATGTTGTTTAAAGCCACTTCTTATGCGACA 1177  
 |||||  
 351 IleLeuThrArgGluGlyTyrProAsnValPheTyrGlyAspTyrTy 367  
 |||||  
 1178 ATCTTGACCGGTGAAGTGGTTATCCAAATGATTTTACGGTACTACTA 1227  
 |||||  
 367 rGlyIleProAsnAspAsnIleSerAlaLysLysAspMetIleAspGlu 384  
 |||||  
 1228 TGGGATTCCTAACGATAACATTCAGCTAAGAAGGATATGATTGATGAGT 1277  
 |||||  
 384 euLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHisAspTyrPhe 400  
 |||||  
 1278 TGCTTGATGCAGCTCAAAATATCGCATATGGCACACACATGACTATTTT 1327  
 |||||  
 401 AspHisTrpAspValValGlyTyrThrArgGluGlySerSerArgPr 417  
 |||||  
 1328 GATCATTTGGGATATCGTTGGATGGACAAAGAGGTACATCTCAGCTCC 1377  
 |||||  
 417 oAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyGlySerLysT 434  
 |||||  
 1378 TAATTCGGGTCTTGCTACTATTATGTCCAATGGTCTCGGAGGATCAAAAT 1427  
 |||||  
 434 rMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThrAspLeuThr 450  
 |||||  
 1428 GGATGTACGTAGGACCAACATGCGAGGACAAACCGTGGACAGATTTAACT 1477  
 |||||  
 451 GlyAsnAsnGlyValSerValThrIleAsnGlyAspGlyTrpGlyGluPh 467  
 |||||  
 1478 GGCAATCACCGCGGTGGTTACGATTAATGGTGTGGCTGGGCGGAATT 1527  
 |||||  
 467 ePheThrAsnGlyGlySerValSerValTyrValAsnGln 480





```

|||||
207 TAACCAAAAGGACGGCTCGTACGAATATGGAAACAAAGCAGAAATAG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
|||||
257 AACGAGCGATTCTGCTTAAAGCGGAACGGGATTCAAGTGATGGCGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
|||||
307 GTTGTATGAACATAAAGCGGAGCTGATTTACCGGAGCGTGTCAAGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
|||||
357 GGTGAAGTGAACCCGCAACACCAACCAAGAAAGTGTCTGGCACTTATC 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
|||||
407 AAATCGAAGCATGGACAGGGTCAATTTCTCGACGTGGCAATCAACAT 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
|||||
457 TCTTCGTTAAATGGCGCTGATCATTTCCGATGGGACGATTGGGACCA 506
167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181
|||||
507 GTCTCGCCAACTCGCAATCGTATTATAGTTTAGAGGAGCGGAAAG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
|||||
557 CATGGGACTGGGAAGTTGACACTGAAATGGGAACATGATTACTTAATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
|||||
607 TATGCAGACTTCGACATGGATGATCATCCAGAAAGTGATTAAACGAAC 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
|||||
657 TTGGGCGCTGTGTACCGGAATACCTTAATTTAGACGGCTTCGCGATGG 706
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
|||||
707 ATCAGTGAACATATATAATTTAGTTCATCGCTGATTGTTAGGCGAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
|||||
757 GTTCGGCGGCAACGGGCAAGAACTCTTTTTCGCGTTGCAGAGTATTGGA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
|||||
807 GAATGACCTAGGGCTTTAGAAAATTTATTAAGCAAAACAAATTTGACGA 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
|||||
857 TGAGCGCTTTGATGTCCTTCATTACAACTTTTCAAGCGTCAAAAT 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl 314
|||||
907 AGTAGCGGAATTTACGACATGAGAACTTTGTTAAATGGAACACTCGTTCA 956
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
|||||
957 ACGTCATCCGAGCGCTGCGGTACGTTTGTGATACACGACGACACAGC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
|||||
1007 CTGGAGAAGCCCTCGAATCGTTCGTTCAAGCGTGGTTAAACCACTAGCT 1056
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl 364
|||||
1057 TATGCAACGATTTTACGAGAGAGCAAGGCTACCCCAAGTGTGTTACGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
|||||

```

```

1107 CGATTATTATGGCATCCCAAGTCACGGTGTCCAAAGCTACCGTCAACAGA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
|||||
1157 TCACCCACCTTTTAAAGCTCGTCACAATATGCTTATGTTAGACAGCAC 1206
398 AspTyrPheAspHisTrpAspValValGlyTyrTrpThrArgGluGlySer 414
|||||
1207 GATTACTTTTCATCATTTGGGATGTAATTTGGCTGGACACGTGAAGAAACGC 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
|||||
1257 ATCTACCCGCAACTCAGGACTTGCACCAATATGCTGATGGTCCAGGTG 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
|||||
1307 GATCAAAATGGAATGATGTTGGCCGTCAGAAAGCTGGCGAAGTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
|||||
1357 GACATGACTGGAACCGCAGTCGCACTGTGACAATTAATCAAGACGCGTG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
|||||
1407 GGGACACTTTTGTCAACGGCGGCTGTGTCCTGATGGGTGAAACGA 1455
seq_name: /SIDS2/gcgdata/geneseq/NA1995.DAT:AAAT00777
seq_documentation_block:
ID AA00777 standard; DNA; 1455 BP.
XX AC AA00777;
XX DT 16-MAR-1996 (first entry)
XX DE Bacillus sp. alkaline alpha-amylase DNA.
XX KW Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile;
XX OS beer; starch; ss.
XX PN Bacillus.
XX PR WO9526397-A1.
XX PD 05-OCT-1995.
XX PF 29-MAR-1995; 95WO-DK00142.
XX PR 03-FEB-1995; 95DK-0000123.
XX PR 29-MAR-1994; 94DK-0000353.
XX PR 03-NOV-1994; 94DK-0001271.
XX PA (NOVO ) NOVO-NORDISK AS.
XX PI Bisgard-frantzen H, Ostergaard PR, Outtrup H, Rasmussen MD;
XX PI Van DER ZEE P;
XX DR WPI; 1995-351318/45.
XX PT New alkaline Bacillus alpha-amylase - used in e.g. detergent
XX PT compns. starch liquefaction, textile desizing, starch modification
XX PT or beer making
XX PS Disclosure; Page 50; 65pp; English.
XX CC This DNA sequence may be expressed recombinantly for the production
XX CC of an alpha-amylase protein. The produced protein is characterized
XX CC by having a specific activity at least 25% higher than the specific
XX CC activity of Termamyl at 25-55 deg C and a pH of 8-10. The enzyme
XX CC can be used in detergent composition for starch liquefaction, the
XX CC production of lignocellulosic materials, e.g. pulp, paper and
XX CC cardboard from waste containing starch, for deinking recycled
XX CC starch-coated, or starch- containing printed paper, to modify

```









```

248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
757 GTAAGAAACGCAACGGGAAAGAAATGTTCTGCTGCTGAATTTGGAA 806
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
264 sAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
807 AAATGATTTAGTGCCTTGGAGAACTATTAAATAAACAACACTGGAAATC 856
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
857 ATTCTGCTTTGATGTCCTCCCTTCATTATATCTTTATAACGCGTCAAT 906
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGI 314
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
907 AGTGGAGCAACTATGATGCGCAAACTTCTTAATGAACGGTGTGTCA 956
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
314 uAlaHisPromethisAlaValThrPheValAspAsnHisAspThrGlnP 331
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
957 AAACATCCATGATGCGCTTAACTTTTGGGATAATCACGATTTCTCAAC 1006
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
331 roGlyGluSerLeuGluSerTyrPValAlaAspTrpPheLysProLeuAla 347
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1007 CTGGGAATCATTTAGATCAATTTGTACAAGAAATGTTTAAAGCCACTTGT 1056
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGI 364
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1057 TATCGGCTTATTTAAACAAGAAACAAGGCTATCCCTGTGCTTCTATGG 1106
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1107 TGACTACTGGAATTCACACATAGTGTCCACGAATGAAGCCCAAGA 1156
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1157 TTGATCCAATCTTAGAGCGCGTCAAAATTTTGCATATGGAACAACAAT 1206
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
398 AspTyrPheAspHisTyrAspValValGlyTyrPheArgGluGlySerSe 414
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1207 GATTTATTTTACCACATCATATATATATCGGATGGACACGTGAAGAAATAC 1256
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1257 CACGATCCCAATTCAGGACTTGGACTATCATGTCGGATGGCGCAGGG 1306
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1307 GAGAGAAATGGATGTACGTAGGCAAAATAAAGCAGGTCAAGTTGGCAT 1356
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1357 GACATACTGGAATAAACCAGGACAGTTACGATCAATCGATGGATG 1406
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
1407 GGCTAATTTTCAGTAATGAGGATCTGTTTCCATTTGGGTGAAACGA 1455
XX ||||| : : : : : : : : : : : : : : : : : : : : : : : :
seq_name: /SDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAx57593
seq_documentation_block:
ID AAX57593 standard; DNA; 1455 BP.
XX
AC AAX57593;
XX
DT 16-JUL-1999 (first entry)
XX
DE Wild type Termamyl(RTM)-like alpha-amylase coding sequence #2.
XX
KW Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction;
KW sweetener; ethanol; ss.
XX
OS Bacillus sp.
XX

```

```

PN W09919467-Al.
XX
PD 22-APR-1999.
XX
PF 13-OCT-1998; 98WO-DK00444.
XX
PR 13-OCT-1997; 97DK-0001172.
XX
PA (NOVO ) NOVO-NORDISK AS.
XX
PI Bisgard-Frantzen H, Borchert TV, Svendsen A;
XX
DR WPI; 1999-277632/23.
XX
PT Variant alpha-amylases - useful as detergents or for textile
PT desizing or starch liquefaction
XX
PS Disclosure; Page 77-78; 93pp; English.
XX
CC This sequence represents the coding sequence for a parent sequence
CC used to generate new variants of a Termamyl-like alpha-amylase with
CC alpha-amylase activity. The variants comprise mutations in 2-6
CC regions/positions relative to an alpha-amylase from either of two
CC Bacillus species in W09526397, B. stearothermophilus, B. licheniformis,
CC B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants
CC are detergent additives for use in detergents for dishwashing, manual
CC or automatic laundry. The variants can also be used for textile desizing
CC or starch liquefaction (e.g. for production of sweeteners or ethanol).
XX
SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

```

```

alignment_scores:
Quality: 1860.50      Length: 483
Ratio: 4.327          Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

alignment_block:
US-09-590-375-1 x AAX57593

Align seg 1/1 to: AAX57593 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
::: ||||| : : : : : : : : : : : : : : : : : : : : : : : :
7 AATGGGCAAAATGGGACGATGATGCAATACTTTGAATGGCACTTGCTAA 56
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
57 TGATGGGAATCACTGGAATAGATTAGAGATGATGCTAGTAATCTAAGAA 106
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
34 sPalaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
:: ||||| : : : : : : : : : : : : : : : : : : : : : : : :
107 ATAGAGGTATAACCGCTATTTTGGATTCCGCTCGCTGGAAAGGACTCG 156
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
157 CAAATGATGTGGGGTATGGAGCTATGATCTTTATGATTTAGGGAAT 206
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACAGTAGTCAATGG 256
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
257 AGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTTATGGGAT 306
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
307 GTAGTGTGAACCATAAAGGAGGAGCTGATGCTACAGAAACAGCTTCTTC 356
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :
357 GTCTGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGGACTACA 406
||| ||||| : : : : : : : : : : : : : : : : : : : : : : : :

```

```
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
407 CAATTGAGCTTGGACTAAGTTTGGATTTTCCAGGGGGAATACATAC 456

151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG1 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
457 TCAGACTTTAAATGGCGTTGGTATCATCTCGATGGTGTAGATTGGGATCA 506

167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
507 ATCAGCACAATTCCAAATCGTATCTACAAATTCGAGGTGATGGTAAGG 556

182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
557 CATGGATTGGGAAGTAGATTCCGGAATAATGGAATATATGATTATTAAAG 606

198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
607 TATGCAGATGTAGATATGATATCGGAGGTAGTAAATGAGCTTAGAAG 656

214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
657 ATGGGAGAAATCGTATACAAATACATAATCTTGATGATTAGATCG 706

231 sPAlaIleLysHisIleProPheTrpTyrTrpSerAspTrpValArgHis 247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
707 ATGCGGTGAACATATTAATAATAGCTTTACACGCTGATTGGTTGACCCAT 756

248 GlnArgAsnGluAlaAspClnAspLeuPheValValGlyGlyTyrTrpLy 264
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
757 GTAAGAAACGCAACGGGAAAGAAATGTTGCTGTGCTGAATTTGGAA 806

264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
807 AAATGATTAGTGCTTGGAGAACTATTTAATAAACAACAACTGGAATC 856

281 eSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
857 ATTCTGTCTTCTGATGTCGCCCTTCATTATAATCTTTATAACGCGTCAAAT 906

298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG1 314
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
907 ACTGGAGGCACTATGACATGCAAACTCTTAATGGAACGGTGTTCAC 956

314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
957 AAAGCATCCAATGCATCGCTAACTTTTGTGGATATACGATTCACAC 1006

331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1007 CTGGGAATCATAGAACTATTGTACAAGAAATGTTTAAAGCCACTTGT 1056

348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrG1 364
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1057 TATGGCTATTATTAACAAGAGAACAAGCTATCCCTCTGCTCTATGG 1106

364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1107 TGACTACTATGGAATTCACACATAGTGTCCAGCAATGAAGCCAAGA 1156

381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1157 TTGATCCAATCTTAGAGCGCGTCAAAATTTTGCATATGGAACACAACAT 1206

398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1207 GATTATTTGACCACTAATAATATCGGATGGACACGTCAGGAAATAC 1256

414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1257 CACGCATCCCAATTCAGGACTTCGCACTATCATGTCGGATGGCCAGGGG 1306
```

```
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1307 GAGAGAAATGGATGTACGTAGGCAAAATAAGCAGTCAAGTTGGCAT 1356

448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1357 GACATAACTGGAAATAAACACGACAGTACGATCAATGCAGATGGATG 1406

464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1407 GCCTAATTTTTCAGTAATAGGAGATCTGTTCCATTTGGGTGAACGA 1455

seq_name: /SIDS2/gcgdata/geneseq/nal1999.DAT:AAx57598
```

seq\_documentation\_block:

ID: AAx57598 standard; DNA; 1455 BP.

XX AC AAx57598;

XX XX 16-JUL-1999 (first entry)

XX DE Wild type Termamyl (RTM)-like alpha-amylase coding sequence #7.

XX KW Variant: Termamyl; alpha-amylase; mutation; Bacillus; detergent;

XX KW dishwashing; laundry; textile; desizing; starch liquefaction;

XX KW sweetener; ethanol; ss.

XX OS Bacillus sp.

XX PN W09919467-A1.

XX XX 22-APR-1999.

XX XX 13-OCT-1998; 98WO-DK00444.

XX XX 13-OCT-1997; 97DK-0001172.

XX XX (NOVO) NOVO-NORDISK AS.

XX XX Bisgard-Frantzen H, Borchert TV, Svendsen A;

XX XX WPI; 1999-277632/23.

XX XX Variant alpha-amylases - useful as detergents or for textile

XX XX desizing or starch liquefaction

XX XX Disclosure; Page 84-85; 93pp; English.

XX CC This sequence represents the coding sequence for a parent sequence used to generate new variants of a Termamyl-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in W09526397, B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of sweeteners or ethanol).

XX SQ Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment\_scores:

Quality: 1860.50 Length: 483

Ratio: 4.327 Caps: 2

Percent Similarity: 89.027 Percent Identity: 66.460

alignment\_block:

US-09-590-375-1 x AAx57598 ..

Align seg 1/1 to: AAx57598 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrGluTrpHisLeuGluAs 17  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

7  AATGGGACAAATGGGACGATGATGCAATACTTGAATGGCACTTGCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaalaLeuSerA 34
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
57 TGATGGGAATCACTGGAATAGATTAAAGATGATGCTAGTAATTAAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProProAlaTrpLysGlyAsnSer 50
   :: |||||:::|||||:::|||||:::|||||:::|||||:::|||||
107 ATAGAGGTATAACCGCTATTGTGGATTCGCCCTGCCCTGCGAAAGGACTCG 156
51 GluAlaaspValGlyTyArgGlyAlaTyArgLeuTyArgLeuGlyLuph 67
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 CAATATGATGGGTATGGGCTATGATCTTTATGATTTAGGGGAATT 206
67 eaSnGlnLysGlyThrValArgThrLysTyArgGlyThrLysAlaGlnLeuG 84
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
207 TAATCAAAAGGGGACGGTCTGCTACTAGTATGGGACACGTAAGTGG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyArgLys 100
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
257 AGCTCGCATCCATCGCTTTAAGAATAATAGCGTTCGAAGTTTATGGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
307 GTAGTGATGAACCATAAAGAGGAGCTGATGCTACAGAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyTr 134
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
357 TGTCGAGGTGAATCCAAATCAACCGGAATCAAGAAATATCTGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyTr 150
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
407 CAATTGAGGCTTGACTAAGTTTGTATTTCCAGGAGGGGTATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
457 TCAGACTTTAAATGGCGTGGTATCATCTTCGATGGTGTAGATTGGGATCA 506
167 nArgTyTrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
507 ATCAGCACAATTCCAAATCGTATCTACAAATTCGAGGTGATGGTAAGG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyArgPtyrLeuLeu 197
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
557 CATGGGATTCGGAAGTAGATTCGGAATAATGGAATATGATTATTAATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
607 TATGCAGATGTAGATATGATATCCGGAGGTAGTAATAGCTTAGAAG 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyArgLeuA 231
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
657 ATGGGAGAATGTATACAAATCATTAATCTGTGATGGATTAGGATCG 706
231 spAlaIleLysHisIleProPheTrpTrpThrSerAspTrpValArgHis 247
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
707 ATCGGTGAGCATATTAATATAGCTTTACACGTGATGCTGTTGACCCAT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyTrpLy 264
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
757 GTAAGAAACCAACGGGAAAGAAATGTTGCTGCTGAATTTGGAA 806
264 sAspAspValGlyAlaLeuGluPheTyArgLeuAspGluMetAsnTrpGlu 281
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
807 AAATGATTTAGGTGCTTGGAGAACTATTAAATAAAACAAACTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyArgPheTyArgAlaSerGln 297
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
857 ATTCTGCTTTGATGTCCTTCATTAATCTTTATACCGCTCAAT 906
298 GlnGlycylSerTyArgMetArgAsnIleLeuArgGlySerLeuValG 314
   :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
907 AGTGGAGGCAACTGACATGGCAAAACTCTTAAATGGAACGGTGTGTCA 956
..

```

```

314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
   : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
957 AAAGCATCCAATGCATGCCGTACTTTTGGATAATACAGATTCTCAAC 1006
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1007 CTGGGAATCATTAGAATCATTTGTACAAGATGGTTTAAGCCACTTGCT 1056
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyTrpProAsnValPheTy 364
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1057 TATGCGCTTATTTTAAACAAGAGAACAAAGGCTATCCCTCTCTCTATGG 1106
364 YAspTyTrpGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1107 TGACTACTATGGAAATCCACACATAGTGTCCAGCAATGAAGCCCAAGA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyAlaTyArgGlyThrGlnHis 397
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1157 TTGATCCAATCTTAGAGCGCGTCAAAATTTGCATATGGAACACACAT 1206
398 AspTyTrpPheAspHisTrpAspValValGlyTrpThrArgGluGlySer 414
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1207 GATATTTTGACCATCATATATATATCGGATGGACACGTGAAGAAATAC 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1257 CACGCATCCAATTCAGGACTTGCAGACTATCATGTGCGATGGCCAGGG 1306
431 lySerLysTrpMetTyArgValGlyArgGlnAsnAlaGlyGlnThrTrp 447
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1307 GAGAGAAATGGATGTAGTAGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1357 GACATACCTGGAATAAACCCAGGAACAGTTACCATCAATCGAGATGATG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyTrpValAsnG 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1407 GCCTAATTTTCAGTAAATGGAGGATCTGTTTCCATTTGGGTCAACGA 1455

```

seq\_name: /SID52/gcgdata/geneseq/geneseq/NA2000.DAT:AAA48481

seq\_documentation\_block:

ID AAA48481 standard; DNA; 1455 BP.

XX AAA48481;

DT 04-SEP-2000 (first entry)

XX DE Bacillus parent Termamyl-like alpha-amylase DNA sequence #2.

XX KW Bacillus; alpha-amylase; washing; textile desizing;  
KW starch liquefaction; saccharification; mutein; mutant;  
KW enzyme stability; hybrid; ss.

XX OS Bacillus sp.

XX FH Key Location/Qualifiers

FT CDS 1..1455

FT /\*tag= a

FT /\*product= "Termamyl-like alpha-amylase"

FT /partial

XX PN WO200029560-A1.

XX PD 25-MAY-2000.

XX PF 16-NOV-1999; 99WO-DK00628.

XX PR 16-NOV-1998; 98DK-0001495.

XX PA (NOVO ) NOVO-NORDISK AS.

XX Svendsen A, Kjaerulff S, Bisgard-Prantzen H, Andersen C;  
XX WPI: 2000-387777/33.  
DR P-PSDB; AAY99603.

XX Variant of parent termamyl-like alpha amylase useful for washing,  
PT textile desizing and starch liquefaction, comprising alterations in one  
PT or more solvent exposed amino acid residues

XX Disclosure; Page 66-67; 80pp; English.

CC The present sequence encodes a parent Termamyl-like alpha-amylase  
CC from which mutants with increased stability at acidic pH, low calcium  
CC concentration and high temperatures have been derived. The sequence was  
CC isolated from a Bacillus genomic DNA library. A variant may contain  
CC mutations in one or more solvent exposed amino acid residues to increase  
CC the overall hydrophobicity of the enzyme or the overall number of  
CC methyl groups in the side chains of exposed residues may be increased.  
CC The mutations can be incorporated by site-directed mutagenesis or by  
CC random mutagenesis. As a result of their increased stability, the  
CC variants are suitable for the industrial processing of starch, i.e.  
CC starch liquefaction and saccharification. They may also be useful for  
CC washing, dishwashing and textile desizing. Hybrid alpha-amylases  
CC comprising partial amino acid sequences derived from two or more  
CC alpha-amylases have also been created in order to increase enzyme  
CC stability.

XX Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment\_scores:  
Quality: 1860.50 Length: 483  
Ratio: 4.327 Gaps: 2  
Percent Similarity: 89.027 Percent Identity: 66.460

alignment\_block:

US-09-590-375-1 x AAA48481 ..

Align seg 1/1 to: AAA48481 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17  
7 AATGGCAAAATGGGACGATGATGCAATACTTTGAATGGCACTTCCTAA 56  
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSera 34  
57 TGATGGGATCACTGGAATAGATTAGAGATGATGCTAGTAATCTAAGAA 106  
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50  
107 ATPAGAGGTATAACCGCTATTTGGATTCCGCTCCGCTGAAAGGACTTCG 156  
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyCluph 67  
157 CAAATATGATGGGGTATGGGACCTATGATCTTTATGATTTAGGGGAAT 206  
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84  
207 TAATCAAAAGGGGCGGTTCGTACTAAGTATGGGACAGCTAGTCAATTGG 256  
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100  
257 AGTCTGCCATCATCGCTTAAAGATAATGGGCTTCAAGTTTATGGGAT 306  
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117  
307 GTAGTGATGAACCAATAAAGGAGGAGCTGATGCTACAGAAAACGTTCTTC 356  
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134  
357 TGTGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGGGACTACA 406

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150  
407 CAATTGAGGCTTGGACTAGTTTGGATTTCAGGGAGGGGTAAATACATAC 456  
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167  
457 TCAGACTTTAAATGGCTTGGTATCATTTCCGATGGTGTAGATTGGATCA 506  
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181  
507 ATCAGCAAAATCCAAATCGTATCTACAAATCCGAGGTGATGGTAAG 556  
182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197  
557 CATGGGATTGGGAAGTAGATTCCGAAAATGGAATATGATTATTAAATG 606  
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214  
607 TATGCAGATGTAGATATGATCCGGAGGTAGTAAATGAGCTTAGAAG 656  
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231  
657 ATGGGGAGNATCGTATACAAATACATTAATCTTGATGGATTTAGGATCG 706  
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247  
707 ATGCGGTGAAGCATATTAATATAGCTTTACACGTGATTGGTTGACCCAT 756  
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrp 264  
757 GTAAGAAACGCAACGGGAAAGAAATGTTGCTGTGTGTAATTTGGAA 806  
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGlu 281  
807 AATGATTTAGTGCTTGGAGAACTATTTAAATAAACAACTGGAATC 856  
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297  
857 ATTCGTCTTTGATGTCCTTCATTAATAATCTTTATAACGGCTCAAT 906  
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314  
907 AGTGGAGGCACTATGACATGCGCAAACTTCTTAATGGAACGGTTGTCA 956  
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGln 331  
957 AAAGCATCAATGCATGCGCTAACTTTTGGATATATCAGATTCTCAAC 1006  
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347  
1007 CTGGGGAATCATTAGAATCATTTGTACAAGATGGTTTAAGCCACTTGC 1056  
348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrG 364  
1057 TATGGCTTATTTTAAACAGAGAACAAGGCTATCCCTCTCTCTCTATGG 1106  
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMet 381  
1107 TGACTACTATGAATTCACACATAGTGTCCAGCAATGAAAGCCACA 1156  
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397  
1157 TTGATCCAATCTTAGAGGCGCTCAAAATTTTGCATATGGAACACACAT 1206  
398 AspTyrPheAspHisTrpAspValValGlyTyrTrpThrArgGluGlySe 414  
1207 GATTATTTTACCACATATAATAATCGGATGGACACGTCGAAAGGAATAC 1256  
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431  
1257 CACGATCCCAATTCAGGACTTGGGACTATCATGTCGGATGGGCCAGGG 1306  
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447

1307 GAGAGAAATGGATGACAGGCAAAATAAGCAGGTCAAGTTGGCAT 1356  
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464  
1357 GACATAACTGGAATAAACACAGGACAGTTACGATCAATCGAGATGGATG 1406  
464 pGlyGluPheThrAsnGlyGlySerValSerValThrValAsnGln 480  
1407 GGCTAAATTTTCAGTAAATGAGGAGCTGTTCCATTTGGGTGAACGA 1455

seq\_name: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT.AAA48486

seq\_documentation\_block:

ID AAA48486 standard; DNA; 1455 BP.

XX AAA48486;

XX 04-SEP-2000 (first entry)

XX Bacillus Termamyl-like alpha-amylase DNA sequence #4.

XX Bacillus; alpha-amylase; washing; textile desizing;  
KW starch liquefaction; saccharification; muten; mutant;  
XX enzyme stability; hybrid; ss.

XX Bacillus sp.

XX Key Location/Qualifiers  
FH 1..1455  
CDS

FT \*tag= a  
FT /product= "Termamyl-like alpha-amylase"  
FT /partial

XX WO200029560-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-DK00628.

XX 16-NOV-1998; 98DK-0001495.

XX (NOVO ) NOVO-NORDISK AS.

XX Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;

XX WPI; 2000-38777/33.

XX P-PSDB; AAY99609.

XX Variant of parent termamyl-like alpha amylase useful for washing,  
PT textile desizing and starch liquefaction, comprising alterations in one  
PT or more solvent exposed amino acid residues

XX Disclosure; Page 70-71; 80pp; English.

XX The present sequence encodes a parent alpha-amylase from which mutants  
CC with increased stability at acidic pH, low calcium concentration and high  
CC temperatures have been derived. The sequence was isolated from a Bacillus  
CC genomic DNA library. A variant may contain mutations in one or more  
CC solvent exposed amino acid residues to increase the overall  
CC hydrophobicity of the enzyme or the overall number of methyl groups in  
CC the side chains of exposed residues may be increased. The mutations can  
CC be incorporated by site-directed mutagenesis or by random mutagenesis. As  
CC a result of their increased stability, the variants are suitable for the  
CC industrial processing of starch, i.e. starch liquefaction and  
CC saccharification. They may also be useful for washing, dishwashing and  
CC textile desizing. Hybrid alpha-amylases comprising partial amino acid  
CC sequences derived from two or more alpha-amylases have also been created  
CC in order to increase enzyme stability.

XX Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

alignment\_scores:

Quality: 1860.50 Length: 483  
Ratio: 4.327 Gaps: 2  
Percent Similarity: 89.027 Percent Identity: 66.460

alignment\_block:

US-09-590-375-1 x AAA48486 ..

Align seg 1/1 to: AAA48486 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17  
7 AATGGGCAAAATGGGACGATGATGCAATCTTGAATGGCACTGCTAA 56  
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA 34  
57 TGATGGGAATCACTGGATAGATGATGCTAGTAATCTAAGAA 106  
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50  
107 ATAGAGGTATACCGCTATTTGGATTCGCTCGCTGGAAGGACTTCG 156  
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67  
157 CAAAATGATGTGGGTATGGAGCTATGATCTTTATGATTTAGGGAAT 206  
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84  
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGTAGCAATGG 256  
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100  
257 AGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAAGTTTATGGGAT 306  
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117  
307 GTAGTGATGAACCATTAAGGAGGAGCTGATGCTACAGAAAACGTTCTT 356  
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyr 134  
357 TGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGGACTACA 406  
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150  
407 CAATTGAGGCTTGACTAAGTTTGATTTCCAGGAGGGGTATACATAC 456  
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167  
457 TCAGACTTAAATGGGTTGGTATCATTTCCGATGGTGTAGATGGGATCA 506  
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181  
507 ATCAGCACAATTCAAAATCGTATCTACAAATTCGAGGATGGTGAAGS 556  
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTrpLeuLeu 197  
557 CATGGGATTTGGGAAGTAGATTCGGAATAATGGAATTTATGATTTAATG 606  
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214  
607 TATGCAGATGATAGATGATGATCATCCGGAGGTAGTAAATGAGCTTAAAG 656  
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231  
657 ATGGGAGAATGATGATACAAATACATAAATCTTGATGGATTTAGGATCG 706  
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247  
707 ATGCGGTGAAGCATATTAATATAGCTTTACACGTGATTTGGTTGACCAT 756  
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGlyTyrTrp 264  
757 GTAAGAACAACGACGGAAGAAAGAAATGTTGCTGTGCTGATTTGGAA 806





```

1154 ATAGAGGTATACCGCTATTGGATTCCGCTGCGCTGGAAGGACCTTCG 1203
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
1204 CAAATGATGTGGGTATGGAGCCCTATGATCTTTATGATTTAGGGAATT 1253
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
1254 TAATCAAAAGGGGCGGTTCGTACTAAGTATGGACACGTAGTCAATTGG 1303
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
1304 AGTCGTCATCCATCGCTTAAAGAAATATGCGGTCAAGTTATGGGGAT 1353
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
1354 GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAAACGTTCTTCG 1403
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
1404 TGTGAGGTGAATCCAAATACCGGAATCAAGAAATATCTGGGGACTACA 1453
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
1454 CAATTGAGGCTTGGACTAAGTTTGCATTTCCAGGAGGGGTATACATAC 1503
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
1504 TCAGACTTTAAATGGCGTTGGTGTATCATTTTCGATGCTGTAGATTGGGATCA 1553
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
1554 ATCAGGACAAATCCAAATCGTATACAAATCCGAGGTGATGGTAAGG 1603
182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197
1604 CATGGGATTCGGAGTAGATTCGGAAATGGAATATGATTTATTTAATG 1653
198 GlySerAsnIleAspPheSerHisProGluValClnAspGluLeuLysAs 214
1654 TATCCAGATGTAGATATGGATATCCCGGAGGTAGTAAATGAGCTTAGAG 1703
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
1704 ATGGGAGAGATGTTATACAAATCAATTAATCTTGATGATTTAGGATCG 1753
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
1754 ATCGGTTGAAGCATATTAATAATAGCTTTACACGCTGATTGGTTGACCCAT 1803
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyLutTrpLys 264
1804 GTAAGAAACCCACGGGAAAGAAATGTTGCTGTCTGAATTTGGAA 1853
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
1854 AAATGATTTAGTGCCTTGGAGAACTATTAAATAAAACAACACTGGAATC 1903
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
1904 ATTCTGTCITTAGTGCCTTCATTTATATCTTTATACGCGCTCAAT 1953
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl 314
1954 AGTGGAGGCAACTATGACATGGCAAACTCTTAAATGGACGCTTGTTC 2003
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
2004 AAAGCATCCAATGCATCGCGTAACTTTTGTGGATAATACGATTCTCAAC 2053
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
2054 CTGGGNAATCATTAGATCATTTGTACAAAGATGGTTTAAAGCCACTTGT 2103

```

```

348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrGl 364
2104 TATGCGGCTATTATTAACAAGACAGACAGGTATCCCTCTGCTTCTATGG 2153
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
2154 TGACTACTATGGAATTCACACATAGTCTCCAGCAATGAAAGCCAAGA 2203
381 leaspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
2204 TTGATCCAAATCTTAGAGCGCGCTCAAAATTTTGCATATGGAACAACAT 2253
398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
2254 GATATTTTGCACCATATATATATTAATCGGATGACACAGTGAAGGAATAC 2303
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
2304 CAGCGATCCCAATTCAGGACTTCGACTATCATGTCGGATGGGCCAGGG 2353
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
2354 GAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 2403
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
2404 GACATAACTGGAATAAACACGAGCAACAGTACATCATCGACATGGATG 2453
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
2454 GGCTAATTTTTCAGTAAATGGAGGATCTGTTCCATTTGGGTGAACGA 2502

```

seq\_name: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT:AA51339

seq\_documentation\_block:

ID AA51339 standard; DNA; 1776 BP.

XX AA51339;

XX 11-NOV-1997 (first entry)

XX Coding sequence for alkaline liquefying alpha-amylase.

XX Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent;  
 starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance;  
 alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent;  
 dish-washing detergent; starch; ds.

XX Bacillus species KSM-AP1378.

XX Key Location/Qualifiers  
 FH 145..1695  
 CDS /\*tag= a

FT /product= alkaline liquefying alpha-amylase

XX WO9700324-A1.

XX 03-JAN-1997.

XX 14-JUN-1996; 96WO-JP01641.

XX 14-JUN-1995; 95JP-0147257.

XX (KAOS ) KAO CORP.

XX Ara K, Hatada Y, Ito S, Kawai S, Ozaki K;

XX WPI; 1997-118708/11.

XX P-PSDB; AAW11326.

XX DNA encoding alkaline liquefying alpha-amylase - useful in  
 dish-washing and laundry detergents for removal of starch dirt

```

794 CATGGACGCGGAAGTAGATATAGAGAACGGCAACTATGATTACCTTATG 843
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
      ::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
844 TATGCAGACATGATATGGATCATCCAGAGTAATCAATCAACTAGAAA 893
214 pTrpGlySerTrpPheThrAspGluLeuAspGlyTyArgLeuA 231
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
894 TTGGGAGATTGGTATACAAATACACTTAATCTPAGATGGATTAGAAATCG 943
231 spAlaIleLysHisIleProPheTrpTrpThrSerAspTrpValArgHis 247
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
944 ATGCTGTGAACATATAAATACAGCTATACGAGAGATTGGCTAAACACAT 993
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTrpLys 264
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
994 GTGGGTAAACACACAGGTAAACCAATGTTTGCAGTTGCAGAAATTTGGAA 1043
264 sAspAspValGlyAlaLeuGluPheTyArgLeuAspGluMetAsnTrpGlu 281
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1044 AAATGACCTTGGTCAATCGAAACATATTTAAATAAAACAAGTTGGAATC 1093
281 etSerLeuPheAspValProLeuAsnTyAsnPheTyArgAlaSerGln 297
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1094 ACTCCGTGTGCAATGCTCTTCATATTAATTTGTACAATGCATCTAAT 1143
298 GlnGlyGlySerTyArgMetArgAsnIleLeuArgGlySerLeuValG 314
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1144 AGTGGTGGCTATTTTCATATGAGAAATATTTTAAATGGTTCTCTCGTACA 1193
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1194 AAACACACCTATACATGCGAGTCACATTTGTTGATAACCATGACTCTCAGC 1243
331 roGlyGlySerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1244 CAGGAGAGCATTTGGAATCCTTTGTTCAATCGTGGTTCAAACCACTGGCA 1293
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyProAsnValPheTyArg 364
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1294 TATGCATTGATCTGCACAGGGAGCAAGGTTACCTTCGCTATTATTACGG 1343
364 yAspTyTyArgIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1344 TGATTTACTACGGTATACCAACTCATGGTGTCTCTCGATGAATCTAAAA 1393
381 leAspGluLeuLeuAspAlaArgGlnAsnTyArgAlaTyArgIleHis 397
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1394 TTGATCCACTCTCGAGGACGTCAAACGTPATGCCTCACGGAACCCAAACAT 1443
398 AspTyPheAspHisTrpAspValValGlyTyThrArgGluGlySerSe 414
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1444 GATTATTTTGTATCATCATGATATATTATCGCTGCACGAGAGAGGGACAG 1493
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1494 CTCCCACCCAAATTCAGGACTTGCAACTATTATGTCGATGGGCCAGGGG 1543
431 lySerIlysrPheTyValGlyArgGluAsnAlaGlyGlnThrTrpThr 447
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1544 GTAATAAATGGATGTATGTCCGGAAACATAAAGCTGCCCAAGTATGAGA 1593
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1594 GATATCACCGGAATAGGTCTGGTCCGTCACCATTAATGCAGATGGTTG 1643
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyArgValAsnGln 480
      :|||||:::|||||:::|||||:::|||||:::|||||:::|||||
1644 GGGGAATTTCACTGTAAACGAGGGGCAGTTTCGGTTGGTGAACCAA 1692
seq_name: /SIPS2/gcgdata/geneseq/geneseq/NA2000.DAT:AAAC6234
seq_documentation_block:

```

seq\_name: /SIDS2/qcdata/qeneseq/qeneseq/NA2000.DAT:AAC66234







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2001, 16:54:37 ; Search time 33.83 Seconds  
(without alignments)  
1050.996 Million cell updates/sec

Title: US-09-590-375-1  
Perfect score: 2687  
Sequence: 1 DGLGTMQYVHLENDGQ.....GDGWGEFTNGGSVYVNVQ 480

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2687	100.0	501	21 AAB14822	Bacillus sp. lique
2	2618	97.4	501	21 AAB14821	Bacillus sp. lique
3	1920.5	71.5	483	21 AAB29340	Bacillus sp. matur
4	1919.5	71.4	483	21 AAB29318	Bacillus sp. matur
5	1915.5	71.3	483	21 AAB29342	Bacillus sp. matur
6	1915.5	71.3	483	21 AAB29343	Bacillus sp. matur
7	1915.5	71.3	483	21 AAB29372	Bacillus sp. matur
8	1914.5	71.3	483	21 AAB29325	Bacillus sp. matur
9	1914.5	71.3	483	21 AAB29341	Bacillus sp. matur
10	1913.5	71.2	483	21 AAB29345	Bacillus sp. matur
11	1913.5	71.2	483	21 AAB29346	Bacillus sp. matur

12	1913.5	71.2	483	21 AAB29348	Bacillus sp. matur
13	1913.5	71.2	483	21 AAB29349	Bacillus sp. matur
14	1913.5	71.2	483	21 AAB29351	Bacillus sp. matur
15	1913.5	71.2	483	21 AAB29352	Bacillus sp. matur
16	1912.5	71.2	483	21 AAB29338	Bacillus sp. matur
17	1912.5	71.2	483	21 AAB29339	Bacillus sp. matur
18	1912.5	71.2	483	21 AAB29344	Bacillus sp. matur
19	1912.5	71.2	483	21 AAB29347	Bacillus sp. matur
20	1912.5	71.2	483	21 AAB29350	Bacillus sp. matur
21	1911.5	71.1	483	21 AAB29337	Bacillus sp. matur
22	1911.5	71.1	485	21 AAB29336	Bacillus sp. matur
23	1910.5	71.1	483	21 AAB29321	Bacillus sp. alpha
24	1910.5	71.1	483	21 AAB29374	Bacillus sp. matur
25	1910.5	71.1	483	21 AAB29375	Bacillus sp. matur
26	1910.5	71.1	485	21 AAB29310	Bacillus sp. matur
27	1909.5	71.1	483	21 AAB29322	Bacillus sp. alpha
28	1909.5	71.1	483	21 AAB29373	Bacillus sp. matur
29	1908.5	71.0	483	21 AAB29377	Bacillus sp. matur
30	1908.5	71.0	483	21 AAB29378	Bacillus sp. matur
31	1908.5	71.0	483	21 AAB29380	Bacillus sp. matur
32	1908.5	71.0	483	21 AAB29381	Bacillus sp. matur
33	1908.5	71.0	483	21 AAB29383	Bacillus sp. matur
34	1908.5	71.0	483	21 AAB29384	Bacillus sp. matur
35	1907.5	71.0	483	21 AAB29370	Bacillus sp. matur
36	1907.5	71.0	483	21 AAB29371	Bacillus sp. matur
37	1907.5	71.0	483	21 AAB29376	Bacillus sp. matur
38	1907.5	71.0	483	21 AAB29379	Bacillus sp. matur
39	1907.5	71.0	483	21 AAB29382	Bacillus sp. matur
40	1906.5	71.0	483	21 AAB29323	Bacillus alpha-amy
41	1906.5	71.0	483	21 AAB29369	Bacillus sp. matur
42	1906.5	71.0	485	21 AAB29332	Bacillus sp. matur
43	1906.5	71.0	485	21 AAB29368	Bacillus sp. matur
44	1905.5	70.9	483	21 AAB29328	Bacillus sp. alpha
45	1905.5	70.9	485	21 AAB29311	Bacillus sp. matur

## ALIGNMENTS

RESULT 1  
AAB14822  
ID AAB14822 standard; protein: 501 AA.  
XX AAB14822;  
XX AAB14822;  
DT 19-DEC-2000 (first entry)  
XX Bacillus sp. liquefying alpha-amyase #2.  
DE Liquefying alpha-amyase; detergent; starch industry; brewing industry;  
KW pharmaceutical industry; food industry; fibre industry.  
XX Bacillus sp.  
XX Bacillus sp.  
PN EPI022334-A2.  
XX  
PD 26-JUL-2000.  
XX  
PF 20-DEC-1999; 99EP-0125399.  
XX  
PR 21-DEC-1998; 98JP-0362487.  
PR 21-DEC-1998; 98JP-0362488.  
XX  
XX (KAOS ) KAO CORP.  
XX  
XX Hagihara H, Kitayama K, Hayashi Y, Igarashi K, Endo K, Ozaki K;  
XX WPI: 2000-516014/47.  
XX N-PSDB: AAA70314.  
XX  
XX New liquefying alkaline amylase, useful in a detergent composition  
XX comprises a residual activity of not less than 70 % when treated under  
XX specific conditions -

```

XX PS Claim 4; Page 17-19; 34pp; English.
XX CC The present sequence is a novel alpha-amylase from Bacillus sp. The
XX CC invention concerns the isolation of two new liquefying alpha-amylases
XX CC from Bacillus sp. strains KSM-K36 and KSM-K38, designated K36 and K38, of
XX CC which this protein is one. The present alpha-amylases are chelating-agent
XX CC resistant and thus are useful in the starch, brewing, fibre,
XX CC pharmaceutical and food industries, and especially as components of
XX CC detergents.
XX SQ Sequence 501 AA;

Query Match 100.0%; Score 2687; DB 21; Length 501;
Best Local Similarity 100.0%; Pred. No. 6.6e-214;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGLNGTMMQYYEWHLENDGQHNRLLHDDAAALSDAGITAIWIPPAYKGNQADVGAYD 60
DB 22 dglngtmmqyyewhlendgqhnrllhddaaalsdagitaiwippaykgnsqadvgyg 81
QY 61 LYDLGEFNQKGTVRTKYGTAKQLERAIGSLKSNIDINVYGDVVMNHKMGADFTFAVOAV 120
DB 82 lydlgefngkgtvrtkygtakqleraigslksndinvygdvvmnhkmgadfteavqav 141
QY 121 NPTNRWQDISGAYTIDAWTGFDSGRNNAYSDFKRWRFHNGVDWDQRYOENHIFR 180
DB 142 nptnrwqdisgaytidawtgdgfsgrnnaysdfkwrwfhngvwdwqryqenhi 201
QY 181 NNNWRVDEENGNYDYLGSNIDFSHPVQDELKDWGSWFTDELDDGYRLDAIKHIP 240
DB 202 nnnwrvdeengnydylgsnidfshpevqdelkdwgsfwtdeldldgyrldaikh 261
QY 241 TSDWVRHQRNEADODLFVVGVEYWKDDVGALFEYLDENWEMSLFDVPLNRYFASQ 300
DB 262 tsdwrhqrneadodlfvvgveywkddvgalefyldennwemslfdvplnryfas 321
QY 301 SYDMRNILRGLSVEAHPHMAVTFVDNHDTPQGESLESWVADWFKPLAYATILTR 360
DB 322 sydmrnilrgslveahphmavtfvndhdtqgesleswvadwfkplayatiltre 381
QY 361 VFYGDYIGIPNDNISAKKMDIDELLDARQNYAGTQHDYFDHWDVVGWTRGSSRP 420
DB 382 vfygdyigipndnisakkmdidelldarqnyagtqhd yfdhwdvvgwtrgssr 441
QY 421 LATIMSGPGGSKWMYVGRQNGAQWTDLTGNGASVTINGDGWGEFFTNNGSVSYV 480
DB 442 latimsgpggskwmyvgrnagqwtldtgnngasvt ingdgwgefftnngsvsy 501

RESULT 2
AAB14821
ID AAB14821 standard; protein; 501 AA.
XX AC AAB14821;
XX CC
XX DT 19-DEC-2000 (first entry)
XX DE Bacillus sp. liquefying alpha-amylase #1.
XX KW Liquefying alpha-amylase; detergent; starch industry; brewing industry;
XX KW pharmaceutical industry; food industry; fibre industry.
XX OS Bacillus sp.
XX PN EP1022334-A2.
XX PD 26-JUL-2000.
XX PF 20-DEC-1999; 99EP-0125399.
XX PP
XX BR 21-DEC-1998; 98JP-0362487.

```

```

PR 21-DEC-1998; 98JP-0362488.
XX PA (KAOS ) KAO CORP.
XX PI Hagihara H, Kitayama K, Hayashi Y, Igarashi K, Endo K, Ozaki K;
XX WPI; 2000-516014/47.
DR N-PSDB; AAA70313.
XX PT New liquefying alkaline amylase, useful in a detergent composition
XX PT comprises a residual activity of not less than 70 % when treated under
XX PT specific conditions -
XX PS Claim 4; Page 14-16; 34pp; English.
XX CC The present sequence is a novel alpha-amylase from Bacillus sp. The
XX CC invention concerns the isolation of two new liquefying alpha-amylases
XX CC from Bacillus sp. strains KSM-K36 and KSM-K38, designated K36 and K38, of
XX CC which this protein is one. The present alpha-amylases are chelating-agent
XX CC resistant and thus are useful in the starch, brewing, fibre,
XX CC pharmaceutical and food industries, and especially as components of
XX CC detergents.
XX SQ Sequence 501 AA;

Query Match 97.4%; Score 2618; DB 21; Length 501;
Best Local Similarity 96.5%; Pred. No. 3.3e-208;
Matches 463; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 DGLNGTMMQYYEWHLENDGQHNRLLHDDAAALSDAGITAIWIPPAYKGNQADVGAYD 60
DB 22 dglngtmmqyyewhlendgqhnrllhddaaalsdagitaiwippaykgnsqadvgyg 81
QY 61 LYDLGEFNQKGTVRTKYGTAKQLERAIGSLKSNIDINVYGDVVMNHKMGADFTFAVOAV 120
DB 82 lydlgefngkgtvrtkygtakqleraigslksndinvygdvvmnhkmgadfteavqav 141
QY 121 NPTNRWQDISGAYTIDAWTGFDSGRNNAYSDFKRWRFHNGVDWDQRYOENHIFR 180
DB 142 npsnrwqdisgaytidawtgdgfsgrnnaysdfkwrwfhngvwdwqryqenhi 201
QY 181 NNNWRVDEENGNYDYLGSNIDFSHPVQDELKDWGSWFTDELDDGYRLDAIKHIP 240
DB 202 nnnwrvdeengnydylgsnidfshpevqdelkdwgsfwtdeldldgyrldaikh 261
QY 241 TSDWVRHQRNEADODLFVVGVEYWKDDVGALFEYLDENWEMSLFDVPLNRYFASQ 300
DB 262 tsdwrhqrneadodlfvvgveywkddvgalefyldennwemslfdvplnryfas 321
QY 301 SYDMRNILRGLSVEAHPHMAVTFVDNHDTPQGESLESWVADWFKPLAYATILTR 360
DB 322 sydmrnilrgslveahphmavtfvndhdtqgesleswvadwfkplayatiltre 381
QY 361 VFYGDYIGIPNDNISAKKMDIDELLDARQNYAGTQHDYFDHWDVVGWTRGSSRP 420
DB 382 vfygdyigipndnisakkmdidelldarqnyagtqhd yfdhwdvvgwtrgssr 441
QY 421 LATIMSGPGGSKWMYVGRQNGAQWTDLTGNGASVTINGDGWGEFFTNNGSVSYV 480
DB 442 latimsgpggskwmyvgrnagqwtldtgnngasvt ingdgwgefftnngsvsy 501

RESULT 3
AAB29340
ID AAB29340 standard; Protein; 483 AA.
XX AC AAB29340;
XX CC
XX DT 09-FEB-2001 (first entry)
XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #10.
XX BR

```







Matches 333; Conservative 62; Mismatches 85; Indels 1; Gaps 1;

Qy 1 DGLNGTMOYEWLENDQGHNRLLHDDAAALSADAGITAIWIPPAYKGNQADVGYGAYD 60  
 Db 3 dgtngtimgyfewvnpdgqhnrlhnaqnlknagitaipwipawkgtsqndvgyggyd 62

Qy 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNIDINVYGDVVMNHKMGADFTFAVOAVOV 120  
 Db 63 lydlgefngkgtvrtkgytkaelerairslkangiqvgydvvmnhkggadttervqavev 122

Qy 121 NPTNRWQDISGAYTIDAWTGFDFSGRNAYSDFKRWRFHFGVWDQO-RYQENHIFRAN 179  
 Db 123 npqnrngvsgtyleavtgnfpgngqhsfkwrwyhfdgtdwdqgrqlsnriykfrg 182

Qy 180 TNWNRVDEENGNDYLLGNSIDFSHPVQDELKDWGSWFTDELDCYRLDAIKHIPFW 239  
 Db 183 kawdvevtengnydylnyadxdmnhpevinelnrgwvwyantlnldgrldavkhqifs 242

Qy 240 YTSWVRHORNEADQDLFVVGGEYWKDDVGALEFYLDENWMSLFDVPLNRYFRASQOG 299  
 Db 243 fmrnwlgvrgtgnlfavaeywkdigalenylskntwmsafdvplhynlyqasnsg 302

Qy 300 GSYDMRNILRGSLEVAHPMHAVTFVDNHDTPQGESLESWADWFKPLAYATILTRGGYP 359  
 Db 303 gnydmrnlngtlvqrhpshtvfdvndhtqgpealesfvvgwfkplayatiltreggyp 362

Qy 360 NVFYGDYGIIPNDNISAKKMDIDELLDARONVAYGTQHDYFDHWDVVGWTRGSSSRPNS 419  
 Db 363 qvfgydygipsdgvpysyrqldpllkarkqaygrqbdyfdhwdvlgwtregashpnps 422

Qy 420 GLATIMSGPGGSKWYVGRQNAQTWTDLTGNNGASVTINGDGMGEFTTNGGSSVSVYN 479  
 Db 423 glatimsdpgpggskwmyvgrkagevwhdtgnrsgtvtinqdgwgqfvnggsvsvwvk 482

Qy 480 Q 480  
 Db 483 r 483

RESULT 6  
 AAB29343  
 ID AAB29343 standard; Protein: 483 AA.  
 AC AAB29343;  
 DT 09-FEB-2001 (first entry)  
 DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #13.  
 KW Alpha-amylase: AAI-6; AAI-10; DSM 12650; DSM 12651;  
 KW alkaline detergent composition; starch liquefaction; textile desizing;  
 KW brewing; baking; ethanol production; starch modification; laundry;  
 KW dishwashing; surface cleaning; mutant; mutein.  
 OS Bacillus sp.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 204  
 FT /note= "Any amino acid other than val"  
 XX WO2000060058-A2.  
 PN 12-OCT-2000.  
 XX 28-MAR-2000; 2000WO-DK00147.  
 XX 31-MAR-1999; 99DK-0000438.  
 PR 13-APR-1999; 99DK-0000489.  
 XX (NOVO ) NOVO NORDISK AS.  
 XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;

PI Bisgard-Frantzen H, Svendsen A, Andersen C;  
 XX WPI: 2000-686938/67.  
 XX New polypeptides having alpha-amylase activity and nucleic acids  
 PT encoding the enzymes, useful as a detergent or a dish wash detergent  
 PT composition, for textile desizing, for liquefaction of starch, or for  
 PT ethanol production -  
 XX Claim 21; Page -: 112pp; English.  
 XX The invention relates to two novel Bacillus alpha-amylases, AAI-6 from  
 CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and  
 CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)  
 CC have improved wash performance in alkaline detergent solutions (pH 9-11)  
 CC and have a temperature optimum in the range 55-65 degrees Celsius at pH  
 CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the  
 CC novel alpha-amylases having increased thermal stability, particularly at  
 CC acidic pH and/or at low Ca2+ concentration. The invention additionally  
 CC encompasses active fragments of the novel alpha-amylases, expression  
 CC constructs and host cells comprising nucleic acids encoding the  
 CC alpha-amylases of the the invention, and the recombinant production of  
 CC these enzymes. The alpha-amylases are useful in a detergent composition  
 CC or a dishwash detergent composition, in a desizing composition,  
 CC for liquefaction of starch, or for ethanol production. In particular,  
 CC the alpha-amylases are useful for textile desizing, starch modification  
 CC in the pulp and paper industry, for brewing or baking, or as laundry,  
 CC dishwashing or hard surface cleaning detergent compositions. They are  
 CC especially useful for removing starchy stains during washing with a  
 CC detergent at alkaline pH. The alpha-amylases are also useful for  
 CC producing drinking or industrial ethanol from starch or whole grains.  
 CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases  
 CC of the invention.  
 CC Note: The present sequence is not shown in the specification, but  
 CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)  
 CC shown on page 105-106.  
 XX Sequence 483 AA;  
 SQ

Query Match 71.3%; Score 1915.5; DB 21; Length 483;  
 Best Local Similarity 69.2%; Pred. No. 3.7e-150;  
 Matches 333; Conservative 62; Mismatches 85; Indels 1; Gaps 1;

Qy 1 DGLNGTMOYEWLENDQGHNRLLHDDAAALSADAGITAIWIPPAYKGNQADVGYGAYD 60  
 Db 3 dgtngtimgyfewvnpdgqhnrlhnaqnlknagitaipwipawkgtsqndvgyggyd 62

Qy 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNIDINVYGDVVMNHKMGADFTFAVOAVOV 120  
 Db 63 lydlgefngkgtvrtkgytkaelerairslkangiqvgydvvmnhkggadttervqavev 122

Qy 121 NPTNRWQDISGAYTIDAWTGFDFSGRNAYSDFKRWRFHFGVWDQO-RYQENHIFRAN 179  
 Db 123 npqnrngvsgtyleavtgnfpgngqhsfkwrwyhfdgtdwdqgrqlsnriykfrg 182

Qy 180 TNWNRVDEENGNDYLLGNSIDFSHPVQDELKDWGSWFTDELDCYRLDAIKHIPFW 239  
 Db 183 kawdvevtengnydylnyadxdmnhpevinelnrgwvwyantlnldgrldavkhqifs 242

Qy 240 YTSWVRHORNEADQDLFVVGGEYWKDDVGALEFYLDENWMSLFDVPLNRYFRASQOG 299  
 Db 243 fmrnwlgvrgtgnlfavaeywkdigalenylskntwmsafdvplhynlyqasnsg 302

Qy 300 GSYDMRNILRGSLEVAHPMHAVTFVDNHDTPQGESLESWADWFKPLAYATILTRGGYP 359  
 Db 303 gnydmrnlngtlvqrhpshtvfdvndhtqgpealesfvvgwfkplayatiltreggyp 362

Qy 360 NVFYGDYGIIPNDNISAKKMDIDELLDARONVAYGTQHDYFDHWDVVGWTRGSSSRPNS 419  
 Db 363 qvfgydygipsdgvpysyrqldpllkarkqaygrqbdyfdhwdvlgwtregashpnps 422

Qy 420 GLATIMSGPGGSKWYVGRQNAQTWTDLTGNNGASVTINGDGMGEFTTNGGSSVSVYN 479

```

Db 423 glatmsdpggskwmyvgrkagevwhdltgnrsgtvtlndqdgvgffvngsvsvvwx 482
QY 480 Q 480
Db 483 r 483

RESULT 7
AAB29372
ID AAB29372 standard; Protein; 483 AA.
XX AC AAB29372;
XX DT 09-FEB-2001 (first entry)
XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:4 mutant #10.
XX KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;
XX KW alkaline detergent composition; starch liquefaction; textile desizing;
XX KW brewing; baking; ethanol production; starch modification; laundry;
XX KW dishwashing; surface cleaning; mutant; mutein.
XX OS Bacillus sp.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 181
XX FT /note= "Any amino acid other than Arg"
XX PN WO2000060058-A2.
XX PD 12-OCT-2000.
XX PF 28-MAR-2000; 2000WO-DK00147.
XX PR 31-MAR-1999; 99DK-0000438.
XX PR 13-APR-1999; 99DK-0000489.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
XX PI Bisgaard-Frantzen H, Svendsen A, Andersen C;
XX DR WPI; 2000-686938/67.
XX PS New polypeptides having alpha-amylase activity and nucleic acids
XX PS encoding the enzymes, useful as a detergent or a dish wash detergent
XX PS composition, for textile desizing, for liquefaction of starch, or for
XX PS ethanol production -
XX PS Claim 21; Page -: 112pp; English.
XX PS
XX CC The invention relates to two novel Bacillus alpha-amylases, AAI-6 from
XX CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and
XX CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
XX CC have improved wash performance in alkaline detergent solutions (pH 9-11)
XX CC and have a temperature optimum in the range 55-65 degrees Celsius at pH
XX CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the
XX CC novel alpha-amylases having increased thermal stability, particularly at
XX CC acidic pH and/or at low Ca2+ concentration. The invention additionally
XX CC encompasses active fragments of the novel alpha-amylases, expression
XX CC constructs and host cells comprising nucleic acids encoding the
XX CC alpha-amylases of the invention, and the recombinant production of
XX CC these enzymes. The alpha-amylases are useful in a detergent composition
XX CC or a dishwash detergent composition, in a desizing composition,
XX CC for liquefaction of starch, or for ethanol production. In particular,
XX CC the alpha-amylases are useful for textile desizing, starch modification
XX CC in the pulp and paper industry, for brewing or baking, or as laundry,
XX CC dishwashing or hard surface cleaning detergent compositions. They are
XX CC especially useful for removing starchy stains during washing with a
XX CC detergent at alkaline pH. The alpha-amylases are also useful for
XX CC producing drinking or industrial ethanol from starch or whole grains.

```

```

CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
CC of the invention.
CC Note: The present sequence is not shown in the specification, but
CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29311)
CC shown on page 109-110.
XX
XX Sequence 483 AA;

```

```

Query Match 71.3%; Score 1915.5; DB 21; Length 483;
Best Local Similarity 69.2%; Pred. NO. 3.7e-150;
Matches 333; Conservative 60; Mismatches 87; Indels 1; Gaps 1;

```

```

QY 1 DGLGTMQVYEHLENDGQHNRLHDDAAALSDAGITAIWIIPPAYKNGSQADVGYGAYD 60
Db 3 dgngtlmqfyewnpvndgqwnrlhnnagnaknagitaipwawkgtsqndvgayd 62
QY 61 LYDLGEFNQKGYTRKYTKAKQLERAIGSLKSNIDINVGDVVMNHKMGADFTAVCAVOV 120
Db 63 lydlgefngkgtvrtkygkkaelerairskangiqyvgdvvmnhkkgadftervqavev 122
QY 121 NPTNRWQDISCAYTIDAWTGFDFSGRNNAYSDFKRWFFHNGVDWQ-RYQENHIFRFAN 179
Db 123 npqnrnqevsgtyqleawtgfnfpgrgndghssfkwrwyhfdgtwdqsgqlanriyxfxg 182
QY 180 TNWNRVDEENGNYDYLLGSNIDFESHPEVQDELKDWGSWFTDELDDLGYELDAIKHIPFW 239
Db 183 kawdewdteingnydylmyadvdmhpveihelnrvwvyantlnldgfrldavkhkfs 242
QY 240 YTSDWVRHORNEADQDLFVVGVEYKDDVGALFEYLDENWEMSLFDVPLNRYFYRASQOG 299
Db 243 fmrdrwlghvrgtgknlfavayekndlgalenyskntwnmsafdvplhynlyqasns 302
QY 300 GSYDMENILRSLVEAHPMHVAFTVDNHDTPQGESLESWADVDFKPLAYATILTREGGYP 359
Db 303 gnydmnllngtlvqchpshavtfvndhdtgpealesfvqgwfplayatiltreggyp 362
QY 360 NVFYGDYGYIPNDNISAKKMDIDELDARQNYAGTQHDYFDHWDVGVWTRGSSSRPNS 419
Db 363 qvfgydygypsdgvsyrgqidpllkarkqayaygrqdyfdhwdvigtregnashpns 422
QY 420 GLATIMSGPGGSKWYVGRQNGAGQTWDTLGNNGASVTINGDGGEGFTNGGVSIVYVN 479
Db 423 glatimsdpggskwmyvgrkagevwhdmtgnrsgtvtlndqdgvgffvngsvsvvwx 482
QY 480 Q 480
Db 483 r 483

```

```

RESULT 8
AAB29325
ID AAB29325 standard; Protein; 483 AA.
XX AC AAB29325;
XX DT 09-FEB-2001 (first entry)
XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:4 mutant, del-D183/G184.
XX KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;
XX KW alkaline detergent composition; starch liquefaction; textile desizing;
XX KW brewing; baking; ethanol production; starch modification; laundry;
XX KW dishwashing; surface cleaning; mutant; mutein.
XX OS Bacillus sp.
XX OS Synthetic.
XX PN WO2000060058-A2.
XX PD 12-OCT-2000.
XX PF 28-MAR-2000; 2000WO-DK00147.

```

```

XX 31-MAR-1999; 99DK-0000438.
PR 13-APR-1999; 99DK-0000489.
XX
PA (NOVO ) NOVO NORDISK AS.
XX
PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
PI Bisgard-Frantzen H, Svendsen A, Andersen C;
XX
DR WPI; 2000-686938/67.
XX
XX New polypeptides having alpha-amylase activity and nucleic acids
PT encoding the enzymes, useful as a detergent or a dish wash detergent
PT composition, for textile desizing, for liquefaction of starch, or for
PT ethanol production -
XX
XX Claim 20; Page -; 112pp; English.
XX
XX The invention relates to two novel Bacillus alpha-amylases, AAI-6 from
CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and
CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
CC have improved wash performance in alkaline detergent solutions (pH 9-11)
CC and have a temperature optimum in the range 55-65 degrees Celsius at pH
CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the
CC novel alpha-amylases having increased thermal stability, particularly at
CC acidic pH and/or at low Ca2+ concentration. The invention additionally
CC encompasses active fragments of the novel alpha-amylases, expression
CC constructs and host cells comprising nucleic acids encoding the
CC alpha-amylases of the the invention, and the recombinant production of
CC these enzymes. The alpha-amylases are useful in a detergent composition
CC for a dishwash detergent composition, in a desizing composition,
CC for liquefaction of starch, or for ethanol production. In particular,
CC the alpha-amylases are useful for textile desizing, starch modification
CC in the pulp and paper industry, for brewing or baking, or as laundry,
CC dishwashing or hard surface cleaning detergent compositions. They are
CC especially useful for removing starchy stains during washing with a
CC detergent at alkaline pH. The alpha-amylases are also useful for
CC producing drinking or industrial ethanol from starch or whole grains.
CC Sequences AAB29318-B29330 represent specific embodiments of the mutant
CC Bacillus alpha-amylases of the invention.
CC Note: The present sequence is not shown in the specification, but
CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29311)
CC shown on page 109-110.
XX
XX Sequence 483 AA;

```

```

Query Match 71.3%; Score 1914.5; DB 21; Length 483;
Best Local Similarity 69.2%; Pred. No. 4.4e-150;
Matches 333; Conservative 60; Mismatches 87; Indels 1; Gaps 1;

QY 1 DGLNGTMMQYEWLHNDGQHNRHDDAALSDAGITAIWPPAYKGNQADYGVAYD 60
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 dgtngtmqyfewvnpdngqwhrlnhnaqnlknagitalwppawkgtsqndvgayd 62
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 LYDIGENQKGTGVTYKTRAQLERATGSLKSDINIVGDVMMHKKGADTEAVQAVQ 120
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 lydigefnqgtvrtkygkkaelralrslkangivgygdvmmhkggadtvrqave 122
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 NPTNRWODISGAYTIDAWTGFDFSGRNAYSDFKWRWFHENGVDWDO-RYOENHIFRAN 179
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 123 npqnrndevsgtyleawtgnfnpgnrqnhsfkwrwyhtdgtwdqdsrqlanrylkfgr 182
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 180 TNNWRVDEENGNDYLLGSNIDFSPHEVDQLKDWCSWFFDELDLCYRLDAIKHHPFW 239
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 183 kawdewdtegnrydylymadvdmhdhevinelnrvgwywviantldgfrldavkhlkfs 242
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 240 YTSQWVRQRNEADQDLFFVGEYKWDVGALFYLDEMNNWMSLFDVPLNFTYRASQOG 299
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 243 fmrldwlgvrgtqtknifavaeykndlgalenylsktnwtmsafdpblyhnylgasns 302
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 300 GSYDMRNLRLGSLVEAHPMIAVTVDNHDTPQGESLSWVADWFKPLAYATILREGGYP 359
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

DB 303 gnydmrnllngtlvgrhpshtvfvdnhdtpqgealesfvqgwkplayatiltreggyp 362
QY 360 NVFYGDYVIGIPNDNISAKKMDIDELLDARQNYAYGTQHDYFDHWDVVGWTRREGSSSRNS 419
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 363 qvfgydgygipsdgvsyrqgidpllkarqyaygrqidyfdhwdvigtreghnashpns 422
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 GLATIMSGPGGSKWMMYVGRQNAQTWTDLTCNGASVYTINGDGMGEFTTNGSGSVSYVN 479
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 423 glatimsdpgpgskwmvyrqkagevwhdmtgnrsgtvtlqngdgwhgffvngsgsvvwwk 482
   |||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 Q 480
DB 483 r 483

```

RESULT 9  
AAB29341  
ID AAB29341 standard; Protein; 483 AA.  
XX  
AC AAB29341;  
XX  
DT 09-FEB-2001 (first entry)  
XX  
DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #11.  
XX  
KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;  
KW alkaline detergent composition; starch liquefaction; textile desizing;  
KW brewing; baking; ethanol production; starch modification; laundry;  
KW dishwashing; surface cleaning; mutant; mutein.  
XX  
OS Bacillus sp.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 204 /note= "Any amino acid other than val"  
FT  
XX WO2000060058-A2.  
XX 12-OCT-2000.  
XX 28-MAR-2000; 2000WO-DK00147.  
XX  
XX 31-MAR-1999; 99DK-0000438.  
XX 13-APR-1999; 99DK-0000489.  
XX  
XX (NOVO ) NOVO NORDISK AS.  
XX  
PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;  
PI Bisgard-Frantzen H, Svendsen A, Andersen C;  
XX  
XX WPI; 2000-686938/67.  
XX  
XX New polypeptides having alpha-amylase activity and nucleic acids  
PT encoding the enzymes, useful as a detergent or a dish wash detergent  
PT composition, for textile desizing, for liquefaction of starch, or for  
PT ethanol production -  
XX  
XX Claim 21; Page -; 112pp; English.  
XX  
XX The invention relates to two novel Bacillus alpha-amylases, AAI-6 from  
CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and  
CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)  
CC have improved wash performance in alkaline detergent solutions (pH 9-11)  
CC and have a temperature optimum in the range 55-65 degrees Celsius at pH  
CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the  
CC novel alpha-amylases having increased thermal stability, particularly at  
CC acidic pH and/or at low Ca2+ concentration. The invention additionally  
CC encompasses active fragments of the novel alpha-amylases, expression  
CC constructs and host cells comprising nucleic acids encoding the  
CC alpha-amylases of the the invention, and the recombinant production of  
CC these enzymes. The alpha-amylases are useful in a detergent composition  
CC or a dishwash detergent composition, in a desizing composition,  
CC for liquefaction of starch, or for ethanol production. In particular,  
CC the alpha-amylases are useful for textile desizing, starch modification  
CC in the pulp and paper industry, for brewing or baking, or as laundry,  
CC dishwashing or hard surface cleaning detergent compositions. They are  
CC especially useful for removing starchy stains during washing with a  
CC detergent at alkaline pH. The alpha-amylases are also useful for  
CC producing drinking or industrial ethanol from starch or whole grains.  
CC Sequences AAB29318-B29330 represent specific embodiments of the mutant  
CC Bacillus alpha-amylases of the invention.  
CC Note: The present sequence is not shown in the specification, but  
CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29311)  
CC shown on page 109-110.

for liquefaction of starch, or for ethanol production. In particular, the alpha-amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for producing drinking or industrial ethanol from starch or whole grains. Sequences AAB29331-B29394 represent the mutant *Bacillus alpha-amylases* of the invention.

CC Note: The present sequence is not shown in the specification, but  
CC is derived from the wild-type *Bacillus* sp. alpha amylase (AAB293310)  
CC shown on page 105-106.

xx  
SQ Sequence 483 AA;

Query Match	71.3%;	Score	1914.5;	DB	21;	Length	483;
Best Local Similarity	69.2%;	Pred.	No. 4.4e-150;				
Matches	333;	Conservative	62;	Mismatches	85;	Indels	1;
Gaps	1;						
QY	1	DCLNGTWMQYEWHLNDGQHNRLLHDDAAALS DAGTAIWIPPAYKGN SQADVYGAYD	60				
Db	3	dgtngtImqyfewvnpndgqtwrlhnnagqlknagitaiwippawkgtsqdvgaygd	62				
QY	61	LYDLGEFNOKCTVRTKYGTAKLERATGSLKSNDIN YGVVMNKKMGADTEAVQAVOV	120				
Db	63	lydlgefndqrgvtvktygtkaelerairslkanglqvyygvvmnhkggadftervqavev	122				
QY	121	NPTNRWODISGAYTIDAWTGDFSGRNNAYSDFKRWRFHFENGVDWDO-RYOENHIFRFAN	179				
Db	123	npqrncqvsgstyeleawtgfnfgrgnqbssfkwrwyhfagtwdgsrqlnrykfcdg	182				
QY	180	TNWNRVRDEENGNYDLLGSNIDFSHPVEQDELKDWSWFTEDEL DCGYRLDA TKHPIFW	239				
Db	183	kawdewdtengnydyImyadomdmhpveInelnrvgwyantInldgfri daykhqfs	242				
QY	240	YTSDWARQRNEAQDQLFVVGYEYWKDDVGALFEFLYDEMWNEMS LFDVPLNFYFRASQQG	299				
Db	243	fmrnwlgvhvrgqtgknlfaevayekndlgalenylskntwtmsafwpllynlyqasnsq	302				
QY	300	GSYDMRNILRGSLVEAHPMIAVTVDNHDTQPGBSLESVADWPKPLAYATILTREGGYP	359				
Db	303	gnydmrnllngtlvrghps havgfvdnhdtpqgealesfvqgwfkplayatiltreggyp	362				
QY	360	NVFYGDYGGTPDNMISA KKMIDELLBARONYAGCTOHDYFDHWDVVGVWTRREGSSRPNS	419				
Db	363	qvfygdyyglpsdgvsyrqqlpbllkardqayagrhdvyfdhwdvjwgwregtnashpns	422				
QY	420	GLATIMSNPGGSKMWYVGRONAGOTWTDLTGNNGASVTINGDGWGGEFFTINGGVSYYVN	479				
Db	423	glatimsdggpggskmwyvgrqakegwwhdtlgnrgtgtInqdgwgqffvngdsvsvwk	482				
QY	480	Q 480					
Db	483	i 483					

RESULT	10	
AAB29345		
ID	AAB29345	standard; Protein; 483 AA.
XX		
AC	AAB29345;	
XX		
DT	09-FEB-2001	(first entry)
XX		
DE	Bacillus	sp. mature alpha-amylase SEQ ID NO:2 mutant #15.
XX		
KW	Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;	
KW	alkaline detergent composition; starch liquefaction; textile desizing;	
KW	brewing; baking; ethanol production; starch modification; laundry;	
KW	diswashing; surface cleaning; mutant; mutein.	
XX		
QS	Bacillus	sp.

OS	Synthetic.
XX	
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 210
FT	/note= "Any amino acid other than Glu"
XX	
XX	WO200060058-A2.
PN	
PD	12-OCT-2000.
XX	
PF	28-MAR-2000; 2000WO-DK00147.
XX	
XX	31-MAR-1999; 99DK-0000438.
PR	13-APR-1999; 99DK-0000489.
XX	
PA	(NOVO ) NOVO NORDISK AS.
PI	
PI	Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
PI	Bisgard-Frantzen H, Svendsen A, Andersen C;
DR	WPT; 2000-686938/67.
XX	
PT	New polypeptides having alpha-amylase activity and nucleic acids
PT	encoding the enzymes, useful as a detergent or a dish wash detergent
PT	composition, for textile desizing, for liquefaction of starch, or for
PT	ethanol production -
XX	
PS	Claim 21; Page -; 112pp; English.
XX	
CC	The invention relates to two novel Bacillus alpha-amylases, AAI-6 from
CC	Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and
CC	nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
CC	have improved wash performance in alkaline detergent solutions (pH 9-11)
CC	and have a temperature optimum in the range 55-65 degrees Celsius at pH
CC	9.0. The invention also relates to mutants (AAB29318-B29394) of the
CC	novel alpha-amylases having increased thermal stability, particularly at
CC	acidic pH and/or at low Ca2+ concentration. The invention additionally
CC	encompasses active fragments of the novel alpha-amylases, expression
CC	constructs and host cells comprising nucleic acids encoding the
CC	alpha-amylases of the the invention, and the recombinant production of
CC	these enzymes. The alpha-amylases are useful in a detergent composition
CC	or a dishwash detergent composition, in a desizing composition,
CC	for liquefaction of starch, or for ethanol production. In particular,
CC	the alpha-amylases are useful for textile desizing, starch modification
CC	in the pulp and paper industry, for brewing or baking, or as laundry,
CC	dishwashing or hard surface cleaning detergent compositions. They are
CC	especially useful for removing starchy stains during washing with a
CC	detergent at alkaline pH. The alpha-amylases are also useful for
CC	producing drinking or industrial ethanol from starch or whole grains.
CC	Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
CC	of the invention.
CC	Note: The present sequence is not shown in the specification, but
CC	is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)
CC	shown on page 105-106.

Query Match	71.2%	Score	1913.5	DB	21	Length	483
Best Local Similarity	69.0%	Pred. No.	5.3e-150				
Matches	332	Conservative	63	Mismatches	85	Indels	1
						Gaps	1

2.







DR WPI; 2000-686938/67.

XX New polypeptides having alpha-amylase activity and nucleic acids

PT encoding the enzymes, useful as a detergent or a dish wash detergent

PT composition, for textile desizing, for liquefaction of starch, or for

PT ethanol production -

XX

PS Claim 21; Page -; 112pp; English.

XX The invention relates to two novel Bacillus alpha-amylases, AAI-6 from

CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and

CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)

CC have improved wash performance in alkaline detergent solutions (pH 9-11)

CC and have a temperature optimum in the range 55-65 degrees Celsius at pH

CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the

CC novel alpha-amylases having increased thermal stability, particularly at

CC acidic pH and/or at low Ca<sup>2+</sup> concentration. The invention additionally

CC encompasses active fragments of the novel alpha-amylases, expression

CC constructs and host cells comprising nucleic acids encoding the

CC alpha-amylases of the the invention, and the recombinant production of

CC these enzymes. The alpha-amylases are useful in a detergent composition

CC or a dishwash detergent composition, in a desizing composition,

CC for liquefaction of starch, or for ethanol production. In particular,

CC the alpha-amylases are useful for textile desizing, starch modification

CC in the pulp and paper industry, for brewing or baking, or as laundry,

CC dishwashing or hard surface cleaning detergent compositions. They are

CC especially useful for removing starch stains during washing with a

CC detergent at alkaline pH. The alpha-amylases are also useful for

CC producing drinking or industrial ethanol from starch or whole grains.

CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases

CC of the invention.

CC Note: The present sequence is not shown in the specification, but

CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)

CC shown on page 105-106.

XX Sequence 483 AA;

SQ

Query Match 71.2%; Score 1913.5; DB 21; Length 483;

Best Local Similarity 69.0%; Pred. No. 5.3e-150;

Matches 332; Conservative 63; Mismatches 85; Indels 1; Gaps 1;

QY 1 DGLNGTMQYWEHLENDGQHNRLHDDAALSDAGITAIWIPPAYKNSQADVGYGAYD 60

DB 3 dgtngtmqyfevwvnpdgqghwnrlhnaqnknagitaipwipawgtsqndvgygayd 62

QY 61 LYDLGEFNQKCTVTKYGTQKALERATGSLKSNINIVGDVVMHKKGADTFEAVQAVQ 120

DB 63 lydlgefnqktvtrkygkaelerairslkangiqyvgdvvmhkhggadftervqavev 122

QY 121 NPTNRWQDFGAYTIDAWTGFDFSGRNNAVSDFKWRWFHFGVDWDO-RYQENHIFRFAN 179

DB 123 npqrnqevsgtyeieawtgnfprgnqshsfkwrwyhfgtdwdsqrlnsriyfrg 182

QY 180 TNMNRVDEENGNDYLLGSNIDFSHPVEQDELKDWGSWFTDELDLGYRLDAIKHIPFW 239

DB 183 kawdewdteengydylmyadvadmmhpveinxlnrvgwyantlnldgrldavkhqfs 242

QY 240 YTSQWVRHORNEADQDLFVGEYKWDVGALFVLDENWEMSLFDVPLNFTFRASQOG 299

DB 243 fmrvnlghvrgtqtknlfavaeywkndlgalenylskntnwtmsafdvplhnylyqasnsg 302

QY 300 GSYDMRNLRGLSVEAHPMHAVTFVDNHDTOPGESLESWADWFKPLAYATILTRGGYP 359

DB 303 gnydmrnlngtlvqrhpshtvtdhndtqpgaelesfvvgwfkplayacilltreggyp 362

QY 360 NVFYGDYIGIPNDNISAKDKMIDLLDARQNYAYCTQHDYFDHVDVVGWTRREGSRRPNS 419

DB 363 qvfgydygippsdgvpsyrqgldplkarqyaygrqhdvfdhwdvlgwtregnasphns 422

QY 420 GLATIMNGPGGSKMVTYGRONACQQTWDTLGNNGASVYTINGDGGWGGFFTNNGSVSVVN 479

DB 423 glatimsdpgpgskmvyvgrkagevwhdtgnrsgtvtlnqdgwggffvngsgsvvkw 482

QY 480 Q 480

DB 483 I 483

RESULT 14

AAB29351

ID AAB29351 standard; Protein; 483 AA.

XX

AC AAB29351;

XX

DT 09-FEB-2001 (first entry)

XX

DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #21.

XX

KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;

KW alkaline detergent composition; starch liquefaction; textile desizing;

KW brewing; baking; ethanol production; starch modification; laundry;

KW dishwashing; surface cleaning; mutant; mutein.

XX

OS Bacillus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 267

FT /note= "Any amino acid other than Lys"

XX

PN WO2000060058-A2.

XX

PD 12-OCT-2000.

XX

PF 28-MAR-2000; 2000WO-DK00147.

XX

PR 31-MAR-1999; 99DK-0000438.

PR 13-APR-1999; 99DK-0000489.

XX

PA (NOVO ) NOVO NORDISK AS.

XX

XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;

PI Bisgard-Franzen H, Svendsen A, Andersen C;

XX

DR WPI; 2000-686938/67.

XX

XX New polypeptides having alpha-amylase activity and nucleic acids

PT encoding the enzymes, useful as a detergent or a dish wash detergent

PT composition, for textile desizing, for liquefaction of starch, or for

PT ethanol production -

XX

PS Claim 21; Page -; 112pp; English.

XX The invention relates to two novel Bacillus alpha-amylases, AAI-6 from

CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and

CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)

CC have improved wash performance in alkaline detergent solutions (pH 9-11)

CC and have a temperature optimum in the range 55-65 degrees Celsius at pH

CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the

CC novel alpha-amylases having increased thermal stability, particularly at

CC acidic pH and/or at low Ca<sup>2+</sup> concentration. The invention additionally

CC encompasses active fragments of the novel alpha-amylases, expression

CC constructs and host cells comprising nucleic acids encoding the

CC alpha-amylases of the the invention, and the recombinant production of

CC these enzymes. The alpha-amylases are useful in a detergent composition

CC or a dishwash detergent composition, in a desizing composition,

CC for liquefaction of starch, or for ethanol production. In particular,

CC the alpha-amylases are useful for textile desizing, starch modification

CC in the pulp and paper industry, for brewing or baking, or as laundry,

CC dishwashing or hard surface cleaning detergent compositions. They are

CC especially useful for removing starch stains during washing with a

CC detergent at alkaline pH. The alpha-amylases are also useful for

CC producing drinking or industrial ethanol from starch or whole grains.

CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases

CC of the invention.

CC Note: The present sequence is not shown in the specification, but  
 CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)  
 CC shown on page 105-106.

XX Sequence 483 AA;

Query Match 71.2%; Score 1913.5; DB 21; Length 483;  
 Best Local Similarity 69.0%; Pred. No. 5.3e-150;  
 Matches 332; Conservative 63; Mismatches 85; Indels 1; Gaps 1;

QY 1 DGLNGTMOYEWHLNDGQHNRHDDAAALSDAGITAIWIPPAYKGNQADVGAYD 60  
 DB 3 dgtngtmqyfevwvndgqhnrlhnaqnlknagitaipwawkgtsqndvgayd 62  
 QY 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKNDINVDVYVNMHKGADFEAVQAVQ 120  
 DB 63 lydlgefngkgtvrtkygkkaelairaisikangiqygdvnmhkggadttervqavev 122  
 QY 121 NPTNRQDISGAYTIDAWTGFDFSGRNNAISDFKRWFFHFGVWDQD-RYQENHIFRFAN 179  
 DB 123 npqnrnqevsgtyeieawtgnfpggrgnqghssfkwrwyhfdgtwdqsrqlsnriykrfg 182  
 QY 180 TNNNRVDEENGNDYLLGSNIDFSPHQDELKDWGSWFTDGLDGYRLDAIKHIPW 239  
 DB 183 kawdevdteengndylymadvdmhpevineinrvgvvyantlnldgfrldavkhqfs 242  
 QY 240 YTSDWVRHQRNEADQDLFVVGWYKDDVGALEFYLDENWMSLFDVPLNRYFRASQOG 299  
 DB 243 fmrnwlgvrgtgnknlfavaywxdlgalenyskntnwsafdvplhynlyqasng 302  
 QY 300 GSYDMRNLRLGSLVAHPHIAVTFVDNHDTPQGESLESWADWFPPLAYATILTRGGY 359  
 DB 303 gnydmrnlrlgtvgrhshavtfvndhdtgpealesfvqgfkplayatiltreqgyp 362  
 QY 360 NYFYGDYGIPIPNDSIAKMDIDELLDARONVAYGTHQDFPHDWDVGVTRGSSRRPNS 419  
 DB 363 qvfygdygipdsqpsyrqqlpdkkarqyaygrqdyfhdwdvlgwtrcgnashpns 422  
 QY 420 GLATIMSGPGSKWYVGRQAGOTWTDLTGNGCASVTINGDGMGEFTNGGVSIVYVN 479  
 DB 423 glatimsdpggskwmyvgrkagewhtdnrsgtvtindgvgqffvngsgsvvwwk 482  
 QY 480 Q 480  
 DB 483 r 483

RESULT 15

AAB29352  
 ID AAB29352 standard; Protein; 483 AA.

XX AC AAB29352;

XX 09-FEB-2001 (first entry)

XX DE Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #22.

XX KW Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;  
 KW alkaline detergent composition; starch liquefaction; textile desizing;  
 KW brewing; baking; ethanol production; starch modification; laundry;  
 KW dishwashing; surface cleaning; mutant; muten.

XX OS Bacillus sp.  
 XX Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 267 /note= "Any amino acid other than Lys"

XX PN WO200060058-A2.

XX PD 12-OCT-2000.

XX 28-MAR-2000; 2000WO-DK00147.  
 XX 31-MAR-1999; 99DK-0000438.  
 PR 13-APR-1999; 99DK-0000489.  
 XX (NOVO ) NOVO NORDISK AS.  
 XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;  
 PI Bisgard-Frantzen H, Svendsen A, Andersen C;  
 XX WPI: 2000-686938/67.  
 XX New polypeptides having alpha-amylase activity and nucleic acids  
 PT encoding the enzymes, useful as a detergent or a dish wash detergent  
 PT composition, for textile desizing, for liquefaction of starch, or for  
 PT ethanol production -  
 XX Claim 21; Page -; 112pp; English.  
 XX The invention relates to two novel Bacillus alpha-amylases, AAI-6 from  
 CC Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and  
 CC nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)  
 CC have improved wash performance in alkaline detergent solutions (pH 9-11)  
 CC and have a temperature optimum in the range 55-65 degrees Celsius at pH  
 CC 9.0. The invention also relates to mutants (AAB29318-B29394) of the  
 CC novel alpha-amylases having increased thermal stability, particularly at  
 CC acidic pH and/or at low Ca<sup>2+</sup> concentration. The invention additionally  
 CC encompasses active fragments of the novel alpha-amylases, expression  
 CC constructs and host cells comprising nucleic acids encoding the  
 CC alpha-amylases of the invention, and the recombinant production of  
 CC these enzymes. The alpha-amylases are useful in a detergent composition  
 CC or a dishwash detergent composition, in a desizing composition,  
 CC for liquefaction of starch, or for ethanol production. In particular,  
 CC the alpha-amylases are useful for textile desizing, starch modification  
 CC in the pulp and paper industry, for brewing or baking, or as laundry,  
 CC dishwashing or hard surface cleaning detergent compositions. They are  
 CC especially useful for removing starchy stains during washing with a  
 CC detergent at alkaline pH. The alpha-amylases are also useful for  
 CC producing drinking or industrial ethanol from starch or whole grains.  
 CC Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases  
 CC of the invention.  
 CC Note: The present sequence is not shown in the specification, but  
 CC is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)  
 CC shown on page 105-106.  
 XX Sequence 483 AA;

Query Match 71.2%; Score 1913.5; DB 21; Length 483;  
 Best Local Similarity 69.0%; Pred. No. 5.3e-150;  
 Matches 332; Conservative 63; Mismatches 85; Indels 1; Gaps 1;

QY 1 DGLNGTMOYEWHLNDGQHNRHDDAAALSDAGITAIWIPPAYKGNQADVGAYD 60  
 DB 3 dgtngtmqyfevwvndgqhnrlhnaqnlknagitaipwawkgtsqndvgayd 62  
 QY 61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKNDINVDVYVNMHKGADFEAVQAVQ 120  
 DB 63 lydlgefngkgtvrtkygkkaelairaisikangiqygdvnmhkggadttervqavev 122  
 QY 121 NPTNRQDISGAYTIDAWTGFDFSGRNNAISDFKRWFFHFGVWDQD-RYQENHIFRFAN 179  
 DB 123 npqnrnqevsgtyeieawtgnfpggrgnqghssfkwrwyhfdgtwdqsrqlsnriykrfg 182  
 QY 180 TNNNRVDEENGNDYLLGSNIDFSPHQDELKDWGSWFTDGLDGYRLDAIKHIPW 239  
 DB 183 kawdevdteengndylymadvdmhpevineinrvgvvyantlnldgfrldavkhqfs 242  
 QY 240 YTSDWVRHQRNEADQDLFVVGWYKDDVGALEFYLDENWMSLFDVPLNRYFRASQOG 299  
 DB 243 fmrnwlgvrgtgnknlfavaywxdlgalenyskntnwsafdvplhynlyqasng 302

Qy 300 GSYDMRILRGSLVEAHMPHMAVTFVDNHDTPQGESLESWADWFKPLAYATILTREGGYP 359  
Db 303 gnydmrllngtlvqrhpshtvfvdnhdtpgealesfvqgwfkplayatiltreggyp 362  
Qy 360 NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTOHDYEDHWDVVGWTRGSSSRPNS 419  
Db 363 qvfyygygipsdgpsyrqqldpilkargqaygrqndyfdhwdvigtregnashpns 422  
Qy 420 GLATIMNGPGGSKWYVGRONAGQTWDLTGNNGASVTINGDGWGEFFFTNGGVSVVVN 479  
Db 423 glatimsdpgpggskwmygrqkagevwhdltgnrsgtvtlnqdgwqffvnggsvsvvkk 482  
Qy 480 Q 480  
Db 483 r 483

Search completed: November 28, 2001, 16:58:04  
Job time: 207 sec

**THIS PAGE BLANK (USPTO)**

OM of: US-09-590-375-1 to: EST.\* out\_format : pfs

Date: Nov 28, 2001 5:37 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

```
-MODEL=framet_p2n.model -DEV=xlh
-O=/cn2.1/USPTO.spool/US09590375/runat_28112001_152037_21046/app_query.fasta_1.1092
-DB=EST -QFMT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-DEPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DLOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USPR=US09590375 -CGNL_1_5378 -NCPU=6
-ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY
-WAIT_THREADS=1
```

Search information block:

Query: US-09-590-375-1

Query length: 480

Database: EST.\*

Database sequences: 11351937

Database length: 1077921985

Search time (sec): 1772.130000

score\_list:

Sequence	Strd	Orig	zScore	EScore	Len	Documentation
gb_gss:AO159619	+	379.50	676.53	1.6e-28	768	! AQ159619 mgxb0001K09r CUGI Rice
gb_est2:BF632036	+	213.00	375.15	9.9e-12	639	! BF632036 NF016C06D71F1039 Drog
gb_est2:BF648578	+	213.00	374.76	1.0e-11	665	! BF648578 NF047G02EC1F1019 Ellic
gb_est2:BF6581061	+	211.00	372.84	1.3e-11	558	! BG581061 EST482791 GVN Medicag
gb_est2:BF637944	+	211.00	372.34	1.4e-11	587	! BF637944 NF041C08PL1F1056 Phosp
gb_est2:BF647599	+	210.00	369.75	2.0e-11	635	! BF647599 NF077E12C1F1098 Ellic
gb_est1:AW709033	+	206.50	367.05	2.8e-11	436	! AW709033 d9b06ne.f1 Neurospora
gb_gss:CNS0100L	-	205.50	360.88	6.2e-11	681	! AL153781 Anopheles gambiae GSS
gb_est2:BF479139	+	198.00	346.78	3.8e-10	712	! BF479139 L48-2786r3 Ice plant I
gb_est2:BF293666	+	196.50	346.88	3.7e-10	533	! BF293666 WHE2156_e10_120ZS Tril
gb_est2:BF253388	+	195.00	342.74	6.3e-10	616	! BF253388 HVSMF0001E16f Hordeum
gb_est2:BF011027	+	191.50	334.17	1.9e-09	771	! BF011027 SB233 Sugar Beet germ
gb_est2:BF073204	+	190.00	332.36	2.4e-09	702	! B1073204 PIP2B_G10 Sugar Beet q
gb_gss:AO159694	+	188.50	329.07	3.6e-09	743	! AQ159694 mgxb0001I08r CUGI Rice
gb_est1:AW223346	+	187.50	328.14	4.1e-09	678	! AW223346 EST300357 tomato fruit
gb_est1:AO083906	+	179.00	315.74	2.0e-08	495	! AO083906 AO083906 Cryptomeria
gb_est2:BG842601	+	178.50	313.83	2.6e-08	548	! BG842601 WHE2151_E01_I01ZS Tril
gb_est2:BF293263	+	178.00	312.42	3.1e-08	577	! BF293263 WHE2151_E01_I01ZS Tril
gb_est1:AW771164	+	177.00	309.81	4.8e-08	679	! AW771164 Str3-C8 Sugar Beet ger
gb_est2:BF292879	+	176.00	308.83	4.9e-08	574	! BF292879 WHE2166_A01_B02ZS Tril
gb_est2:BF292945	+	176.00	308.81	4.9e-08	575	! BF292945 WHE2166_F10_L20ZS Tril
gb_est2:BF522066	+	175.00	308.07	5.4e-08	515	! BF522066 EST425835 potato leave
gb_est2:BF293088	+	173.50	306.15	6.9e-08	474	! BF293088 DGL_50_H11.bl_A002 Dar
gb_gss:AO159867	+	173.00	301.51	1.2e-07	694	! AQ159867 mgxb0002G08r CUGI Rice
gb_est1:AO084730	+	164.00	288.48	6.6e-07	492	! AO084730 AO084730 Cryptomeria
gb_gss:CNS0001B	+	162.50	286.50	8.6e-07	456	! AL091025 Arabidopsis thaliana q
gb_est1:BE358599	+	162.00	283.10	1.3e-06	588	! BE358599 DGL_30_F01.bl_A002 Dar
gb_est1:BE357274	+	162.00	282.81	1.4e-06	606	! BE357274 DGL_148_D01.bl_A002 Da
gb_est2:BG890669	+	160.50	277.87	2.6e-06	599	! BG890669 EST516520 ESTD Solanum
gb_est1:BE436615	+	160.00	279.28	2.2e-06	760	! BE436615 EST407733 tomato break
gb_est1:BE360090	+	159.00	277.20	2.8e-06	615	! BE360090 DGL_61_G11.bl_A002 Dar
gb_est1:BE460819	+	157.00	275.56	3.5e-06	501	! BE460819 EST412238 tomato break
gb_est2:BF293754	+	149.50	261.41	2.1e-05	527	! BF293754 WHE2154_F04_L08ZS Tril
gb_est1:BE436573	+	149.00	259.87	2.6e-05	562	! BE436573 EST407651 tomato break
gb_est1:AW725250	+	149.00	259.23	2.8e-05	600	! AW725250 1116 Ptfirg2 Pinus taed
gb_est2:BI173333	+	149.00	258.39	3.1e-05	654	! BI173333 RE162933 Sprime Re Dros
gb_est2:BF293134	+	148.50	261.11	2.2e-05	451	! BF293134 WHE2164_A02_A04ZS Tril
gb_est2:BF293375	+	148.50	259.46	2.7e-05	534	! BF293375 WHE2157_E10_D19ZS Tril
gb_est2:BF640409	+	147.00	259.33	2.8e-05	409	! BF640409 NF089G07EC1F1056 Ellic
gb_est1:BE360816	+	147.00	256.14	4.2e-05	567	! BE360816 DGL_67_F11.bl_A002 Dar

```
gb_est2:BF632387 + 147.00 251.64 7.5e-05 899 ! BF632387 HVSMBa0016111f Hord
gb_est2:BG598624 - 146.50 252.63 6.6e-05 740 ! BG598624 EST503524 CSTS Sola
gb_gss:AZ686517 - 144.50 246.62 0.0001 943 ! AZ686517 ENTJR71TR Entamoeba
gb_est1:AV834958 + 144.00 250.08 9.1e-05 603 ! AV834958 AV834958 K. Sato un
gb_est2:BI265677 + 144.00 249.33 0.0001 651 ! BI265677 NF083B09IN1F1077 In
```

seq\_name: gb\_gss:AO159619

```
seq_documentation_block: 768 bp DNA GSS 09-SEP-1998
LOCUS AO159619
DEFINITION mgxb0001K09r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0001K09r, DNA sequence.
```

ACCESSION AQ159619

VERSION AQ159619.1 GI:3556644

KEYWORDS GSS.

SOURCE Magnaporthe grisea.

ORGANISM Magnaporthe grisea

REFERENCE 1 (bases 1 to 768)

AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,

Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Magnaporthe grisea

Genome

JOURNAL Unpublished (1998)

COMMENT Contact: Dean RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson University, Clemson, SC 29634

Tel: 864 656 5737

Fax: 864 656 4293

Email: rdean@clemson.edu

Seq primer: GGAACACGCTATGACCATG

Class: BAC ends

High quality sequence stop: 400.

Location/Qualifiers

FEATURES

source

1. .768

/organism="Magnaporthe grisea"

/strain="70-15"

/db\_xref="taxon:148305"

/clone="mgxb0001K09r"

/clone\_lib="CUGI Rice Blast BAC Library"

/tissue\_type="Protoplasts"

/lab\_host="E. coli DH10B"

/note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;

Rice blast is one of the most devastating fungal diseases

of rice world wide. It is a filamentous ascomycete with

a haploid genome (n=7) of approximately 40 Mbp. Rice

blast is an important model fungal pathogen for studying

numerous aspects of the fungal-host interaction. In

order to facilitate genome wide analysis, a BAC library

containing 9216 clones with an average insert size of 130

kbp was constructed. This library represents greater

than 25X genome coverage. High density colony filters

are available upon request."

BASE COUNT 169 a 189 c 244 g 163 t 3 others

ORIGIN

alignment\_scores:

Quality: 379.50

Ratio: 2.654

Percent Similarity: 57.661

Length: 248

Gaps: 5

Percent Identity: 35.484

alignment\_block:

US-09-590-375-1 x AQ159619 ..

Align seg 1/1 to: AQ159619 from: 1 to: 768

41 TrpIleProProAlaTyrIysGlyAsnSerGlnAla...AspValGlyTy 56

|||||

2 TGGATCCACCGCGCTGCAAGGGCGCGCTGTGCTGTGAGCAACGGCTA 51

```

56 rGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrV 73
52 CGAGCTCTAGCATCTGTATGATCGGCCAGTTGACCAAGAGCTCCA 101
73 alArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySer 89
102 AGCGACCAAGTGGGCGCCAGCACCGACCTGACGAGCTCGTCGCGGCC 151
90 LeuLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLy 106
152 GCGGGGACGCGCGCATGTAGATCTGTTTGATGCGGTGTAACCAACA 201
106 sMetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnPro 123
202 GCGCGCGCGGATTCACCGAGCGAGTGTTCGACGAGGTTGACCCAG 251
123 hrAsn..... 124
252 AGGGTTGTGCGCCTGATGTTGCGATGGGCAAGATGCGGTGTATCGCAT 301
125 .....ArgTrpGln..AspIleSerGlyAla 132
302 CGCGGCTGACAAAGAAAGACTGCCAGCGTACTCTGTATGTTGCAGATCG 351
133 TyrThr.....IleAspAlaTrpThrGlyPheAs 142
352 CGCANACAGGTGCATGCGCGCGGAGAGATCGAGGCGGTGGACCAAGTTCGA 401
142 pPheSerGlyArgAsnAlaTyrSerAspPheLysTrpArgTrpPheH 159
402 CTTCACAGGCGCATGATGATCAATATAGTCCCGCGGTGGAACAAGCGC 451
159 isPheAsnGlyValAspTrpAspGlnArgTyrGlnGluAsnHisIlePhe 175
452 ATTTACAGGTGCGACTATGACAATGCAACTGTTGAAAGAGCCATATGG 501
176 ArgPheAlaAsnThrAsnTrpAsnTrpArgValAspGluGluAsnGlyAs 192
502 TTGTTTTCAGGGCAAGAAGTGGCGGAGGATGTGAACGGGAGTTTGGTAA 551
192 nTyrAspTyrLeu..... 196
552 CTATGACTACTGTGAGTCTCGAGTCTCGAGATGCGGAGATGTTTCTCGAGGTGCC 601
197 .....LeuGlySerAsnIleAspPheSerHis 205
602 GGCCTAAATTTGATGCTATCAGAATGTTGCAGACCTAGATCATTCACAT 651
206 ProGluValGlnAspGluLeuLysAspTrpGlySerTrpPheThrAspGI 222
652 TCTGAAGTCAGGAGTGTCTTAAAGTGGCCCAAGTGGCTCAACGATCA 701
222 uLeuAspLeuAspGlyTyrArgLeuAspAlaIleLysHisIle 236
702 AATGTTGCTTGGCGGCTTTCGCTGGACGCCGTTTAAAGCCATA 744
seq_name: gb_est2:BF632036

```

```

seq_documentation_block: 639 bp mRNA EST 19-DEC-2000
LOCUS BF632036
DEFINITION NF016C06DT1F1039 Drought Medicago truncatula cDNA clone NF016C06DT
5', mRNA sequence.
ACCESSION BF632036
VERSION BF632036.1 GI:11896194
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 639)
AUTHORS Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,

```

```

TITLE
JOURNAL
COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 639 Std Error: 0.00
Plate: 016 row: C column: 06
Seq primer: TCACACAGGAACACAGCTATGAC.
FEATURES
Location/Qualifiers
1..639
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF016C06DT"
/clone_lib="Drought"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
timepoints."
BASE COUNT 187 a 127 c 126 g 199 t
ORIGIN

```

```

alignment_scores:
Quality: 213.00 Length: 233
Ratio: 1.718 Gaps: 13
Percent similarity: 53.219 Percent identity: 30.043
alignment_block:
US-09-590-375-1 x BF632036 ..
Align seg 1/1 to: BF632036 from: 1 to: 639

```

```

7 MetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAs 23
76 CTCTTTTCAGGGATTCACCTGGGAGTCAAGTACAAAGAGGAGGTACAA 125
23 nArgLeuHisAspAlaAlaLeuSerAspAlaGlyIleThrAlaI 40
126 CTCTTTGAGAACCTCATCTCGACCTAGCAAAATGCTGGAATTACACATG 175
40 letrPileProProAlaTyrLysGlyAsnSerGlnAlaAspValGlyTyr 56
176 TTTGGCTTCCTCT.....CCATCTCAAAGTGTGGTCTCTCAAGGATAT 219
57 GlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrVa 73
220 CTTCAGGAGAGCTTTATGATCTTGAT..... 246
73 lArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerL 90
247 .GCATCAAAATACGGTTCAAAAGATGACCTAAAAGTCACTAATTGCAGCTT 295
90 euLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLys 106
296 TCAAAGATAAAGAACTAATGTGTCTAGCTGACATAGTAGTCAACCATAGA 345
107 MetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnProth 123
346 .....AC 347
123 rAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpThrG 140
348 AGCAGAAAGAAAAGATGATAGAGGCATCTATTGCCTC..... 384
140 lyPheAspPheSerGlyArgAsnAsnAlaTyrSerAspPheLysTrpArg 156

```

```

REFERENCE
AUTHORS

```



```

SOURCE          barrel medic.
ORGANISM         Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE       1 (bases 1 to 558)
AUTHORS         Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town
                  ,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
TITLE           ESTs from one month old nitrogen-fixing root nodules of Medicago
                  truncatula, 2001
JOURNAL         Unpublished (2001)
COMMENT         Contact: Carroll P. Vance
                  Department of Agronomy and Plant Genetics
                  University of Minnesota
                  411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
                  Tel: 612 625 5715
                  Fax: 651-649-5058
                  Email: vance004@maroon.tc.umn.edu
                  University of Minnesota name: M382117e TIGR sequence name:
                  MTCCDD78TK More information is available at: http://www.medicago.org
                  Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
FEATURES       Location/Qualifiers
                1..558
                /organism="Medicago truncatula"
                /cultivar="genotype Al7"
                /db_xref="taxon:3880"
                /clone="pGVN-63M12"
                /clone_lib="GVN"
                /tissue_type="N2-fixing root nodules"
                /dev_stage="effective root nodules harvested one month
                post inoculation with Sinorhizobium meliloti"
                /lab_host="E. coli strain XL0LR"
                /note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
                XhoI; cDNA was prepared from polyA+ enriched RNA from
                effective root nodules harvested one month post
                inoculation with Sinorhizobium meliloti. The cDNA was
                directionally ligated into the Uni-ZAP XR vector from
                Stratagene and packaged using Gigapack III Gold packaging
                extracts. Plasmids containing cDNA inserts were excised
                from the recombinant lambda-ZAP phage using Ex-Assist
                helper phage and propagated in XL0LR cells."
                BASE COUNT 169 a 110 c 115 g 163 t 1 others
                ORIGIN
                alignment_scores:
                Quality: 211.00 Length: 231
                Ratio: 1.744 Gaps: 12
                Percent Similarity: 52.381 Percent Identity: 29.004
                alignment_block:
                US-09-590-375-1 x BG581061 ..
                Align seg 1/1 to: BG581061 from: 1 to: 558
                7 MetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAs 23
                ::::||||| ::::||||| ::::||||| ::::||||| ::::|||||
                25 CTCTTTTCAGGAGTTCACCTGGAGTCAAGTACAAAGAGGAGGTGATACAA 74
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
                23 nAAGLeuHisAspAlaAlaAlaLeuSerAspAlaGlyIleThrAlaI 40
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
                75 CTCTTTTGAAGACCTCATCTCCTGACCTACCAATGCTGGAATTTACACATG 124
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
                40 leftrpleProAlaTyrLysGlyAsnSerGlnAlaAspValGlyTyr 56
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
                125 TTTGGCTTCTCTCT.....CCATCTCAAAGTGTGGTCTCTCAAGGATAT 168
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
                57 GlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrVa 73
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
                169 CTTCACGAGGAGACTTTTATGATCTTGAT..... 195
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
                73 lAAGThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerL 90
                :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

```

196 .GCATCAAAATACGGTTCAAAGATGACCTAAAGTCACTAATTCAGCTT 244
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
90 eulYSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLys 106
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
245 TCAAGATAAAGAAATCAATGTCTAGCTGACATAGTATGATCAACCATAGA 294
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
107 MetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnProTh 123
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
295 .....AC 296
123 rAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpThrG 140
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
297 AGCAGAAAGAAAGATGATAGAGGCATCTATTGCTC..... 333
140 lYPheAspPheSerGlyArgAsnAlaTyrSerAspPheLysTrpArg 156
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
334 .....TTTGAGGT.....GGGACTCTGATTCAAAACCTTGAT 366
157 Trp.PheHis.PheAsnGlyValAspTrpAspGlnArgTyrGlnGluAsn 172
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
367 TGGGGCCCATCTTTTCAT.....TTGCAAGATGA 395
173 His...IlePheArgPheAlaAsnThrAsnTrpAsnTrpArg.ValaspG 188
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
396 CACTGCTTATTCAGA.....TGGCACTGGAACCTCGATA 430
188 luGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsnIleAspPheSer 204
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
431 GTGGAGAGGC.....TATCAAGCTGCACCTGACATGATCATCTC 471
205 HisProGluValGlnAspGluLeuLysAspTrpGlySerTrpPheThrAs 221
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
472 AATCCTCAAGTACAAAGAGTTATCTGAATGGATGAATTTGGTCAAAAC 521
221 pGluLeuAspLeuAspGlyTyrArgLeuAspAlaIle 233
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
522 TGAATTTGGATNTCTGGTGGAGATTGATTTTGTG 558
seq_name: gb_est2:BF637944
seq_documentation_block: 587 bp mRNA EST 19-DEC-2000
LOCUS BF637944
DEFINITION NF041C08PL1F1056 Phosphate starved leaf Medicago truncatula cDNA
clone NF041C08PL 5', mRNA sequence.
ACCESSION BF637944
VERSION BF637944.1 GI:11902102
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 587)
AUTHORS Liu,J., Scott,D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mharrison@noble.org
Insert Length: 587 Std Error: 0.00
Plate: 041 row: C column: 08
Seq primer: TCACACAGGAACACGCTATGAC.
FEATURES Location/Qualifiers
                1..587
                /organism="Medicago truncatula"

```



name: qb est2:BF647599

seq. documentation block:			
LOCUS	BF647599	635 bp	EST
DEFINITION	NF077E12C1F1098	Elicited cell culture	Medicago truncatula cDNA
	clone NF077E12EC 5',	mRNA sequence.	

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 635)  
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research  
Unpublished (2000)  
Contact: Dixon RA

RODRIGUES-JEREZ, I., SCOLL, A. D., HALLIS, A. R., GONZALES, R. A., BELL, C. J., FLORES, H. R., INMAN, J. T., WELLER, J. W. and MAY, G. D.

JOURNAL  
UNPUBLISHED (2000)  
CONTACT: Dixon RA  
COMMENT

2510 34th NOBLE PARKWAY, ARLINGTON, OR 97021, USA  
Tel: 580 221 7302

insert length: 055 , Std Error: 0.00  
Plate: 077 row: E column: 12

```
source
1: 1000
/organism="Medicago truncatula"
```

/tissue\_type="Cell cultures derived from root tissues"

cell wall extracts equivalent to 50ug/ml glucose in the

BASE COUNT	183 a	129 c	125 g	197 t	1 others
BASE COUNT	183 a	129 c	125 g	197 t	1 others

alignment\_scores:

.....

Align seg 1/1 to: BF647599 from: 1 to: 635

95 TGGGAGTCAAGTAACAAGGAGGATGGTACAACTCTTTGAAGAACCTCAT 144

[illegible]

```

145 TCCTGACCTAGCAATGCTGGAATTACACATGTTGGCTTCTCCT.... 190
46 yrlYsGlyAsnSerGlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyr 62
   :::::||||| ::::| |||||
191 ..CCATCTCAAAAGTGTGGTCTCTCAAGGATATCTCCAGGAAGACTTAT 238
   :::::|||||
63 AspLeuGlyGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyTh 79
   |||||
239 GATCTTGAT.....GCATCAAAATACGGTTC 264
79 rLysAlaGlnGluArgAlaIleGlySerLeuLysSerAsnAspIleA 96
   ||| :::::|||||
265 AAAAGATGACCTAAAGTCACTTAATGAGCTTTCAAGAGAAAGAAATCA 314
   :::::|||||
96 snValTyrGlyAspValValMetAsnHisLysMetGlyAlaAspPheThr 112
   || :::::|||||
315 ATTCTCTAGCTGACATAGTGATCAACCATAGA..... 346
113 GluAlaValGlnAlaValGlnValAsnProThrAsnArgTrpGlnAspII 129
   ||| :::::|||||
347 .....ACAGCAGAAAGAAAGATGA 366
129 eSerGlyAlaTyrThrIleAspAlaTyrThrGlyPheAspPheSerGlyA 146
   ||| ||| :::::|||||
367 TAGAGGCATCTATTGCCCTC.....TTTGAAGGT. 394
146 rgAsnAsnAlaTyrSerAspPheLysTrpArgTrp.PheHis.PheAsnG 162
   :::::|||||
395 .....GGGACTCCCTGATTCAAAACTTATTGGGGCCCATCTTTTCAT. 435
162 lyValAspTrpAspGlnArgTyrGlnGluAsnHis.....IlePheArgPhe 177
   ||| :::::|||||
436 .....TTGCAAGATGCACACTGCTTATTTCAGA... 462
178 AlaAsnThrAsnTrpAsnTrpArg.ValAspGluGluAsnGlyAsnTyrA 194
   ||| :::::|||||
463 .....TGGCACTGAAACCTCGATAGTGGAGAGGCG..... 493
194 spTyrLeuLeuGlySerAsnIleAspPheSerHisProGluValGlnAsp 210
   :::::|||||
494 ..TATCAAGCTGCACCTGACATGATGATCATCTCAATCTCAAGTACAAAA 541
211 GluLeuLysAspTrpGlySerTrpPheThrAspGluLeuAspLeuAspG1 227
   ||||| :::::|||||
542 GAGTTATCTGAATGATGATTGGCTCAAAACTGAAATGGATTTTCTGG 591
227 yTyrArgLeuAspAlaIleLys 234
   ||||| :::::|||||
592 TTGGAGATTGATTGTTGTCAAA 613

```

seq\_name: gb\_est1:AW709933

seq\_documentation\_block: 436 bp mRNA EST 25-APR-2000  
LOCUS AW709933 Neurospora crassa evening cDNA library Neurospora crassa  
DEFINITION cDNA clone d9b06ne 5', mRNA sequence.

ACCESSION AW709933

VERSION AW709933.1 GI:7599010

KEYWORDS EST.

SOURCE Neurospora crassa.

ORGANISM Neurospora crassa

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

AUTHORS 1 (bases 1 to 436)

JOURNAL Sordariales; Sordariaceae; Neurospora.

COMMENT Zhu,H., Lai,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.

Two Neurospora crassa EST Databases

Other\_ESTs: d9b06ne.r1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

Department of Chemistry and Biochemistry

Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

We anticipate the future release of the cDNA clones to the Fungal  
Genetics Stock Center

Seq primer: Universal Forward Primer

High quality sequence stop: 424.

#### FEATURES

##### Source

```

1. 436
   /organism="Neurospora crassa"
   /strain="Strain 30-7 (bd; A)"
   /db_xref="taxon:5141"
   /clone="d9b06ne"
   /cclone.lib="Neurospora crassa evening cDNA library"
   /tissue_type="tissue harvested following 22hr growth in
   dark"
   /note="Vector: pBluescript SK-; Site_1: XbaI; Site_2:
   EcoRI; See: Bell-perdersen.D., et al. PNAS 93:13096,1996.
   5' end of cDNA cloned into XbaI site of pBluescript; 3'
   end of cDNA cloned into EcoRI site of pBluescript"

```

BASE COUNT 82 a 159 c 93 g 102 t  
ORIGIN

##### alignment\_scores:

Quality: 206.50 Length: 119  
Ratio: 2.950 Gaps: 2  
Percent Similarity: 58.824 Percent Identity: 41.176

##### alignment\_block:

US-09-590-375-1 x AW709933 ..

Align seg 1/1 to: AW709933 from: 1 to: 436

```

257 PheValValGlyGluTyrTrpLysAspValGlyAlaLeuGluPheTy 273
   ||| :::::|||||
80 TTATCGTGGGGAATACATGCGCGGAAGATTCCGAGTTTTCGCGGGTA 129
   :::::|||||
273 rLeuAspGluMetAsnTrpGluMetSerLeuPheAspValProLeuAsnT 290
   ||| :::::|||||
130 CATCGAATTTATGCACACCGCTGTCTCTCTTCGACGTGCAATTAGTCT 179
   :::::|||||
290 yTyrAsnPheTyrArg.....AlaSerGln 297
   |||||
180 CCAACTTCTCCCGCATCTTTAGTTTCGAAACACCTCCAGCCCTCC 229
   :::::|||||
298 GlnGlyGly.....SerTy 302
   |||||
230 ACCGGTGGTGGTGGTCTCCCGGATCAGTACGGCAGCGCGACAC 279
   :::::|||||
302 rAspMetArgAsnIleLeuArgGlySerLeuValGluAlaHisPrometh 319
   ||| :::::|||||
280 CGACCTCGCACCTTATTTCGACGACACCTCTGCAATCTGGAAACCGCAC 329
   :::::|||||
319 isAlaValThrPheValAspAsnHisAspThrGlnProGlyGluSerLeu 335
   ::||| :::::|||||
330 AC CGCGTCTCTTGTGTTAACCGACACACAAAAAGCGCAATCGCTC 379
   ::||| :::::|||||
336 GluSerTrpValAlaAspTrpPheLysProLeuAlaTyrAlaThrIle 352
   ||| :::::|||||
380 GAAACGCCCATAGCGCCCTTCTTCATGCCCTCGCTATTCGCTCATCTT 429
   ::|||
352 uThrArg 354
   |
430 ACTTCGC 436

```

seq\_name: gb\_gss:CNS0100L

seq\_documentation\_block:

CNS0100L 681 bp DNA GSS

LOCUS Anopheles gambiae GSS T7 end of clone 26N13 of NotreDamel library

DEFINITION Anopheles gambiae GSS T7 end of clone 26N13 of NotreDamel library

from strain PEST of Anopheles gambiae (African malaria mosquito),

genomic survey sequence.

ACCESSION AL153781

14-JUN-2001

```
VERSION      AL153781.1  GI:7014700
KEYWORDS     GSS.
SOURCE       African malaria mosquito.
ORGANISM     Anopheles gambiae
             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
             Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
             Culicoidae; Anopheles.
REFERENCE    1 (bases 1 to 681)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
             - Web : www.genoscope.cns.fr)
REFERENCE    2 (bases 1 to 681)
AUTHORS     Roth,C.W., Brey,P.T., Ke.Z., Collins,F.H. and Weissbach,J.
TITLE       Direct Submission
JOURNAL     Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
COMMENT     This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.
FEATURES     Location/Qualifiers
             source
             1..681
             /organism="Anopheles gambiae"
             /strain="PEST"
             /db_xref="taxon:7165"
             /clone="26N13"
             /clone_lib="NotreDame1"
             /note="end : T7"
BASE COUNT   147 a 131 c 182 g 216 t 5 others
ORIGIN

alignment_scores:
  Quality: 205.50      Length: 102
  Ratio: 2.704         Gaps: 2
  Percent Similarity: 74.510  Percent Identity: 46.078

alignment_block:
US-09-590-375-1 x CNS0100L/rev ..
Align seg 1/1 to reverse of: CNS0100L from: 1 to: 681

6  ThrMetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrp 22
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 ACCCTGCTGCAATCTTCCACTGGTACTACCCGACGCGGCAAACTGTG 255

22 pAsnArgLeuHisAspAspAlaAlaLeuSerAspAlaGlyIleThra 39
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 GCAGGAGCGCGCGAGCGCGCCGACCTGGCGAACTGGCGATTACCG 205

39 laIleTrpIleProAlaTyrLysGlyAsnSerGlnAla....AspVal 54
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 ACCGTGTG..CTGCGCGCTGCCACAGGCGGTCTCGCGCGCTACTCCGTC 156

55 GlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysG1 71
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
155 GGCTACGATACTAGGACTGTTCGATCTCGCGGAATTGACCAGAAAGG 106

71 yThrValArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleG 88
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
105 CAGCGTGGCCACCAATAACGGCGACAGCGCGCTCGAACACGCTCGCG 56

88 lySerLeuLysSerAsn...AspIleAsnValTyrGlyAspValValMetA 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
55 CAACCTCTCGCGCGAACACGGCGTGGGACACTCTACGACGTGGTGTCA 6

104 snHis 105
|||||
5 ACCAC 1

seq_name: gb_est2:BF479139
```

```
seq_documentation_block:
LOCUS      BF479139          712 bp      mRNA      EST      20-FEB-2001
DEFINITION L48-2786T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-2786
5', mRNA sequence.
ACCESSION  BF479139
VERSION    BF479139.1  GI:11549966
KEYWORDS   common ice plant.
SOURCE     Mesembryanthemum crystallinum
           Mesembryanthemum crystallinum
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
REFERENCE  1 (bases 1 to 712)
AUTHORS    Cushman, J.C.
TITLE      An expressed sequence tag database for the common ice plant,
           Mesembryanthemum crystallinum
JOURNAL    Unpublished (1997)
COMMENT    Contact: Cushman JC
           Department of Biochemistry
           University of Nevada
           MS200, Reno, NV 89557-0014, USA
           Tel: 775-784-1918
           Fax: 775-784-1650
           Email: jcushman@unr.edu
           PCR Primers
           FORWARD: T7
           BACKWARD: T3
           Plate: L48-28 row: H column: 2
           Seq primer: T3
           High quality sequence stop: 350
           POLYA=No.
FEATURES     Location/Qualifiers
             source
             1..712
             /organism="Mesembryanthemum crystallinum"
             /db_xref="taxon:3544"
             /clone="L48-2786"
             /clone_lib="Ice plant Lambda Uni-Zap XR expression library
             , 48 hours NaCl treatment"
             /tissue_type="Leaf, 48 h 0.4M NaCl"
             /dev_stage="Six week old"
             /note="vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
             EcoRI; Site_2: XhoI"
BASE COUNT   217 a 124 c 170 g 201 t
ORIGIN

alignment_scores:
  Quality: 198.00      Length: 240
  Ratio: 1.523         Gaps: 13
  Percent Similarity: 54.167  Percent Identity: 28.333

alignment_block:
US-09-590-375-1 x BF479139 ..
Align seg 1/1 to: BF479139 from: 1 to: 712

181 AsnTrpAsn....TrpArgVal.....AspGluG1 189
|||||:|||||:|||||:|||||:|||||:
39 GATTGGGTGCTTGGTTCATTTCGAGGAGCAGACACAAATACTCCGATGG 88

189 uAsnGlyAsnTyrAsp.....TyrLeuLeuGlySerAsnIleA 202
|||||:|||||:|||||:|||||:|||||:
89 TTCTGGAAACCTTGATCTAGCTGGAGCTGGTTATGCTGCTCCAGATTGG 138

202 spPheSerHisProGluValGlnAspGluLeuLysAspTrpGlySerTrp 218
|||||:|||||:|||||:|||||:|||||:|||||:
139 ATCATTGTGAATCCAAGAGTACAAAGAGAGATTATCAGATTGGATTGG 188

219 PheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaIleLysHi 235
|||||:|||||:|||||:|||||:|||||:|||||:
189 CTTAAGACTGAAATTGGTTTCGATGGAGATTGATTTGTTTAAGGG 238
```



```

129 eSerGlyAlaTyrThrIleAspAlaTrpThrGlyPheAspPheSerGlyA 146
    ||| ||| |||
292 CCGGGGCATCTACTGCATC..... 310
146 rGAsnAsnAlaTyrSerAspPheLysTrpArgTrpPheHisPheAsnGly 162
    |||: |||: |||:
311 .....TTGAGGGC 319
163 .....ValAspTrp..... 165
320 GGCACCGGACGGCGCTCGACTGGGGCCCCACATGATCTGCCGGGA 369
166 .AspGlnArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsnT 182
    |||: |||: |||:
370 CGACCGCCCTACGCCGAGCG..... 391
182 rPAsnTrpArgValAspGluAsnGlyAsn.....TyrAsp 194
    :|||: |||
392 .....ACGGCAACCGCGACACCGCGCGCGC 418
195 TyrLeuLeuGlySerAsnIleAspPheSerHisProGluValGlnAspG1 211
    :|||: |||: |||:
419 TTCGGGGCGCCCGGACATCGACACCTCAACCGCGCGCTCCAGAAGGA 468
211 uLeuLysAspTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyT 228
    |||: |||: |||:
469 GCTCGTCAGTGGCTCACTGGCTCAGGACCGAGCTCGGCTTCGACGGCT 518
228 yrArgLeuAsp 231
    :|||: |||
519 GCGCTTCGAC 529

```

seq\_name: gb\_est2:BF253388

```

seq_documentation_block: 616 bp mRNA EST 23-FEB-2001
LOCUS BF253388 HVSMEf0001E16f Hordeum vulgare seedling root EST library HVCDNA0007
DEFINITION (etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEf0001E16f, mRNA sequence.

```

ACCESSION BF253388

VERSION BF253388.2 GI:13116477

KEYWORDS EST.

SOURCE barley.

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
; Triticeae; Hordeum.

1 (bases 1 to 616)

Wing,R., Clouse,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu  
Y., Anderson,H., Dale,J., Henry,D., Kermode,S., Palmer,M., Rambo  
T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and  
Wood,T.

Development of a genetically and physically anchored EST resource

for barley genomics

Unpublished (2000)

On Nov 16, 2000 this sequence version replaced gi:11182589.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: twing@clemson.edu

Seq primer: AATTAACCTCTACTAAAGG

High quality sequence stop: 517.

Location/Qualifiers

source

1. .616 /organism="Hordeum vulgare"

/cultivar="Morex"

/db\_xref="taxon:4513"

/clone="HVSMEf0001E16f"

/clone\_lib="Hordeum vulgare seedling root EST library

HVCDNA0007 (etiolated and unstressed)"

/tissue\_type="Seedling root"

/lab\_host="TJC121"

/note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI; For  
more details on library preparation and sequence analysis  
see http://www.genome.clemson.edu/projects/barley/ To  
order a clone see http://www.genome.clemson.edu/orders"

BASE COUNT 112 a 215 c 183 g 106 t

ORIGIN

alignment\_scores:

Quality: 195.00 Length: 229

Ratio: 1.639 Gaps: 9

Percent Similarity: 51.965 Percent Identity: 25.764

alignment\_block:

US-09-590-375-1 x BF253388 ..

Align seg 1/1 to: BF253388 from: 1 to: 616

```

7 MetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAs 23
  :|||: |||: |||:
51 CTCTTTCAGGGGTTCACTGGAGTGGTGAAGCAGAGCGCGGTGGTA 100
  :|||: |||: |||:
23 nArgLeuHis.....AspAspAlaAlaAlaLeuSerAspAlaG 36
  :|||: |||: |||:
101 CAACATGATGATGGCAAGTCGACGATCGCGCT.....GCG 141
  :|||: |||: |||:
36 lyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSerGlnAla 52
  :|||: |||: |||:
142 GAGTCACCCACGTCGTGGTGCACCG.....CCGTCGACATCCGTCCTCC 185
  :|||: |||: |||:
53 AspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnG1 69
  :|||: |||: |||:
186 AACGAAGGTTACATCCCTGGTGGTGTACGACATCGAC..... 224
  :|||: |||: |||:
69 nLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuGluArgA 86
  :|||: |||: |||:
225 .....GCGTCCAGTACGGCAACCGCGGAGCTCAAGTCGC 261
  :|||: |||: |||:
86 laIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAspValVal 102
  :|||: |||: |||:
262 TCATCGCGCGCTCCACGCAAGGGCGTGCAGGCATCGCCGACATCGTC 311
  :|||: |||: |||:
103 MetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAlaValG1 119
  :|||: |||: |||:
312 ATCAACCCCGCTGC...GCCGACTAC..... 335
  :|||: |||: |||:
119 nValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleA 136
  :|||: |||: |||:
336 .....AAGGATAGCGCGGCATCTACTGCATC. 362
  :|||: |||: |||:
136 spAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyrSerAsp 152
  :|||: |||: |||:
363 .....TTCAGGGCGGCACCTCCGACGGCGC..... 389
  :|||: |||: |||:
153 PheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGlnArgTy 169
  :|||: |||: |||:
390 .....CTCGACTGGGGCCC..... 404
  :|||: |||: |||:
169 rGlnGluAsnHisIlePheArgPheAlaAsnThrAsnTrpAsnTrpArgV 186
  :|||: |||: |||:
405 .....CACATGATCTGTCCGACGACACCAATACTCCGATGGCA 444
  :|||: |||: |||:
186 alAspGluGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsnIleAsp 202
  :|||: |||: |||:
445 CGCAAAACCTCGACACCGGAGCGGACTTCGCGCGCGCGCCGACATCGAC 494
  :|||: |||: |||:
203 PheSerHisProGluValGlnAspGluLeuLysAspTrpGlySerTrpPh 219
  :|||: |||: |||:
495 CACCTTAACGACCGGGTCCAGCGGAGGTCAAGAGTGGCTCTCTGGCT 544
  :|||: |||: |||:

```





Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;



407 lyTrpThrArgGluGly 412  
                  :::||||:::|  
614 ACAAAAGCCGAAAGGGA 630

**THIS PAGE BLANK (USPTO)**

Seq. cont.	Strd Orig	ZScore	E-Score	Len	Documentation
gb_pat:AX137670	+ 2687.00	3735.50	8.6e-200	1753	AX137670 Sequence 3 from Patent
gb_pat:AX137672	+ 2618.00	3639.99	1.8e-194	1625	AX137672 Sequence 5 from Patent
gb_pat:AX037040	+ 1910.50	2654.94	1.3e-139	1458	AX037040 Sequence 3 from Patent
gb_pat:AX037042	+ 1905.50	2647.97	3.2e-139	1458	AX037042 Sequence 3 from Patent
gb_pat:AR027255	+ 1860.50	2585.28	1.0e-135	1455	AR027255 Sequence 5 from Patent
gb_pat:AR049518	+ 1860.50	2585.28	1.0e-135	1455	AR049518 Sequence 5 from Patent
gb_pat:AR104349	+ 1860.50	2585.28	1.0e-135	1455	AR104349 Sequence 5 from Patent
gb_pat:AR129913	+ 1860.50	2585.28	1.0e-135	1455	AR129913 Sequence 10 from Patent
gb_pat:AR129918	+ 1860.50	2585.28	1.0e-135	1455	AR129918 Sequence 15 from Patent
gb_pat:AR137884	+ 1860.50	2585.28	1.0e-135	1455	AR137884 Sequence 10 from Patent
gb_pat:AR137888	+ 1860.50	2585.28	1.0e-135	1455	AR137888 Sequence 14 from Patent
gb_pat:AR143214	+ 1860.50	2585.28	1.0e-135	1455	AR143214 Sequence 10 from Patent
gb_pat:AR143218	+ 1860.50	2585.28	1.0e-135	1455	AR143218 Sequence 14 from Patent
gb_pat:EI2445	+ 1853.50	2573.83	4.4e-135	1776	EI2445 DNA encoding liquefaction
gb_pat:AB008763	+ 1853.50	2573.79	4.4e-135	1786	AB008763 Bacillus sp. gene for
gb_pat:AR027254	+ 1835.50	2550.44	8.7e-134	1455	AR027254 Sequence 4 from Patent
gb_pat:AR049517	+ 1835.50	2550.44	8.7e-134	1455	AR049517 Sequence 4 from Patent
gb_pat:AR104348	+ 1835.50	2550.44	8.7e-134	1455	AR104348 Sequence 4 from Patent
gb_pat:AR129912	+ 1835.50	2550.44	8.7e-134	1455	AR129912 Sequence 9 from Patent
gb_pat:AR129917	+ 1835.50	2550.44	8.7e-134	1455	AR129917 Sequence 14 from Patent
gb_pat:AR137883	+ 1835.50	2550.44	8.7e-134	1455	AR137883 Sequence 9 from Patent
gb_pat:AR137887	+ 1835.50	2550.44	8.7e-134	1455	AR137887 Sequence 13 from Patent
gb_pat:AR143213	+ 1835.50	2550.44	8.7e-134	1455	AR143213 Sequence 9 from Patent
gb_pat:AR143217	+ 1835.50	2550.44	8.7e-134	1455	AR143217 Sequence 13 from Patent
gb_pat:AR087556	+ 1835.50	2550.42	8.7e-134	1458	AR087556 Sequence 11 from Patent
gb_pat:AX036928	+ 1813.50	2519.76	4.5e-132	1438	AX036928 Sequence 1 from Patent
gb_pat:AX036930	+ 1813.50	2519.76	4.5e-132	1458	AX036930 Sequence 3 from Patent
gb_pat:BACAMYG6	+ 1802.50	2500.22	5.5e-131	2397	M18662 Bacillus sp. (alkalophilic
gb_pat:EI12201	+ 1726.50	2398.06	2.7e-125	1539	EI12201 DNA encoding a heat-and
gb_pat:A23402	+ 1723.50	2394.39	4.3e-125	1419	A23402 B.licheniformis gene for
gb_pat:A27772	+ 1723.50	2393.49	4.3e-125	1449	A27772 Alpha amylase coding se
gb_pat:A47677	+ 1723.50	2393.88	4.6e-125	1539	A47677 Sequence 1 from Patent
gb_pat:A17930	+ 1723.50	2392.66	5.4e-125	1777	A17930 Alpha amylase gene. 4/1
gb_pat:I24553	+ 1723.50	2392.66	5.4e-125	1777	I24553 Sequence 33 from patent
gb_pat:I83686	+ 1723.50	2392.66	5.4e-125	1777	I83686 Sequence 16 from patent
gb_pat:AR008294	+ 1723.50	2392.01	5.8e-125	1920	AR008294 Sequence 1 from patent
gb_pat:AR032774	+ 1723.50	2392.01	5.8e-125	1920	AR032774 Sequence 1 from patent
gb_pat:AR052144	+ 1723.50	2392.01	5.8e-125	1920	AR052144 Sequence 1 from patent
gb_pat:AR087550	+ 1723.50	2392.01	5.8e-125	1920	AR087550 Sequence 1 from patent
gb_pat:AR129915	+ 1723.50	2392.01	5.8e-125	1920	AR129915 Sequence 12 from patent

```

375 CAGCGCGATGTTGGGTACGGTGCATACCATCTTTATGATTTAGGAGATT 424
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
|||||
425 CAATCAAAAGGCTACTGTTCAACGAATACAGGAACCTAAGCCACAGCTTG 474
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
|||||
475 AACGAGCTATTGGTCCCTTAATCTAATGATATCAATGATATACGGAGAT 524
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
|||||
525 GTCGTGATGAATCAATAAATGGGAGCTGATTTTACGGAGGCGAGTCAAGC 574
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
|||||
575 TGTTCAAGTAATCAACGAATCGTTGCAGGATATTTTCAGGTSCCTACA 624
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
|||||
625 CGATTGATCGGTGGACGGGTTTCGACTTTTTCAGGGCGTAAACAGCGCTAT 674
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
|||||
675 TCAGATTTTAAGTGGAGATGGTCCATTTTAATGCTGTTGACTGGGAICA 724
167 nArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsnTrpAsnT 184
|||||
725 GCGCTATCAAGAAATCATATTTTCCGCTTTGCAATACGAACGTGAAC 774
184 rPArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsn 200
|||||
775 GCGGAGTGGATGAAGAGACGGTAATTTATGATTACCTGTAGGATCGAAT 824
201 IleAspPheSerHisProGluValGlnAspGluLeuLysAspTrpGlySe 217
|||||
825 ATCGACTTTAGTCATCCAGAAGTACAAGATGAGTTGAAGGATTTGGGTAG 874
217 rTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaIleL 234
|||||
875 CTGCTTTTACCGATGAGTGTAGATTGGATGTTATCGTTTATGATGCTATTA 924
234 yHisIleProPheTrpTyrThrSerAspTrpValArgHisGlnArgAsn 250
|||||
925 AACATATTCATTCTGGTATACATCTGATTTGGTTCGGCATCAGCGCAAC 974
251 GluAlaAspGlnAspLeuPheValValGlyLutryTrpLysAspAspVa 267
|||||
975 GAAGCAGATCAAGATTTATTTGTCGTAGGGAATATTGGAAGGATGACGT 1024
267 lGlyAlaLeuGluPheTyrLeuMetAsnTrpGluMetSerLeuP 284
|||||
1025 AGTGTCTCCGAATTTTATTTAGATGAATGAATGGGAGATGTCCTAT 1074
284 heAspValProLeuAsnTyrAsnPheTyrArgAlaSerGlnGlnGlyGly 300
|||||
1075 TCGATGTCCACTTAATATAATTTTACGGGCTTCACACACAGGTGGA 1124
301 SerTyrAspMetArgAsnIleLeuArgGlySerLeuValGluAlaHisPr 317
|||||
1125 AGCTATGATATCGTAAATATTTTACGAGGATCTTTAGTAGAAGCGCATCC 1174
317 oMetHisAlaValThrPheValAspAsnHisAspThrGlnProGlyGluS 334
|||||
1175 GATGATGATGCTGCTGATTTTAAAGCCACTTGCTTATGCGACA 1224
334 erLeuGluSerTrpValAlaAspTrpPheLysProLeuAlaTyrAlaThr 350
|||||
1225 CATTAGAGTCATGGTGTGCTGATTTTAAAGCCACTTGCTTATGCGACA 1274
351 lIleLeuThrArgGluGlyTyrProAsnValPheTyrGlyAspTyrTy 367
|||||
1275 ATTTTGACGCGTGAAGGTGGTTATCCAAATGATTTTACGGTGATTA 1324

```

```

367 xGlyIleProAsnAspAsnIleSerAlaLysLysAspMetIleAspGluL 384
|||||
1325 TGGGATTCCTAACGATAACATTTTCAGCTAAAAAGATATGATTGATGAGC 1374
384 euLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHisAspTyrPhe 400
|||||
1375 TGCTTGATGCACGTCACAAATTTACGCATATGCACGACGACATGACTATTT 1424
401 AspHisTrpAspValValGlyTrpThrArgGluGlySerSerSerArgPr 417
|||||
1425 GATCATTTGGGATGTTGTAGGATGGACTAGGAAAGGATCTTCTCCACACC 1474
417 oAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyGlySerLysT 434
|||||
1475 TAATTCAGGCTTGGCAGCTATTATGTCGAATGGACCTGGTGGTTCCAAGT 1524
434 rPMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThrAspLeuThr 450
|||||
1525 GGATGTATGTAGGACGTGAGAATGCAGGACAAACATGGACAGATTTAACT 1574
451 GlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTrpGlyGluPh 467
|||||
1575 GGTAATAACGAGCGCTCCGTTACAATTAATGCGCATGGATGGGCGCAATT 1624
467 ePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
|||||
1625 CTTTACGAATGGAGGATCTGATCCGTGACGTGACGTGAACCAA 1664

```

seq\_name: gb\_pat:AX137672

seq\_documentation\_block: 1625 bp DNA PAT 30-MAY-2001

LOCUS AX137672 Sequence 5 from Patent EP1065277.

DEFINITION AX137672

ACCESSION AX137672

VERSION AX137672.1 GI:14273855

KEYWORDS

SOURCE

ORGANISM

Bacillus sp. KSM-K36.

Bacillus sp. KSM-K36

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Bacillus.

REFERENCE

1 (bases 1 to 1625)

Endo, K., Igarashi, K., Hayashi, Y., Hagihara, H. and Ozaki, K.

Mutant alpha-amylases

Patent: EP 1065277-A 5 03-JAN-2001;

Kao Corporation (JP)

FEATURES

Location/Qualifiers

1..1625

/organism="Bacillus sp. KSM-K36"

/db\_xref="taxon:161485"

40..102

40..1545

/note="unnamed protein product"

/codon\_start=1

/transl\_table=1

/protein\_id="CAC39918.1"

/db\_xref="GI:14273856"

/translation="MKRWVYMLAVLFPPSVVVDGLNGTMMQYEWHLNDGQHNW

RLHDDAEALSNAGITAIWIPYKGNQSOADVGAYLDYLDGFEFNOKGTVTKYGTKA

QLERATGSLKSNIDINVYGVNMHKLGADETAQVAVQVNPSPNWDISGVYRTIDATP

GFDPGNNAYSDPKWRFHFNQVNDWQVQENHLEFATNNNRVDENGNYDYLL

GSNIDFSHPVQBELKDWGSFTDELDGTRLDALIKHIFWTSDMVRHQRSEADOD

LFVVGYEKDDVGALEFYLDENMNSFLDVLNRYFRASKQGGSDYMRNIRLGSIV

EAHPITHAVTFVNDHTQPGESLESWADFKPLAYATILRREGYPNVFGDYVYIPN

DNISAKMDIDEILDARQNYAGTQHDYFDHWDIVGWTREGTSRPNGLATIMSNCP

GGSKWYVGOOHAGQTTDLTGNHAASVTINGDWGGEFFTINGGSVSVYVNVQ"

103..1542

/product="unnamed"

mat\_peptide 468 a 264 c 416 g 477 t

BASE COUNT

ORIGIN

alignment\_scores:





1407 GGGACAATTTTCTCAACGGTGGTCCGTCTCCGTATGGCTGAAACGA 1455

seq\_name: gb\_pat:AX037042

seq\_documentation\_block: 1458 bp DNA PAT 16-NOV-2000  
LOCUS AX037042 Sequence 3 from Patent WO0060058.

DEFINITION AX037042

ACCESSION AX037042

VERSION AX037042.1 GI:11226474

KEYWORDS

SOURCE

ORGANISM

Bacillus sp.

Bacillus sp.

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 1458)

Borchert, T.V., Hoeck, L.H., Outtrup, H., Svendsen, A., Andersen, C.,

Bisgaard-Frantzen, H., Nielsen, B.R. and Nielsen, V.S.

Polypeptides having alkaline alpha-amylase activity and nucleic

acids encoding same

Patent: WO 0060058-A 3 12-OCT-2000;

NOVONORDISK AS (DK)

FEATURES

Location/Qualifiers

1..1458

/organism="Bacillus sp."

/db\_xref="taxon:1409"

1..1455

<1..1458

/note="unnamed protein product"

/codon\_start=1

/transl\_table=11

/protein\_id="CAC16494.1"

/db\_xref="GI:11226475"

/translation="HHDSNGTNGIMQVFEMNPNVDGQWMLHNNALNKNAGITAIWI

PPWKGTSNDYGVGAYDLYDLGEFNOKGTVRTKYTKAELERAIRSLKANGIOVYGD

VVMNHKGADFTERVOAEVNPQNRNOEVSQVQIEATGTFNPGRGNOHSSFKRWY

HFDCDWDSDSROLANRIYKFRDGRKANDWEYDTEGNVDYLMYADVDMHPVEVIELN

RMGVNTNTNDLGGFLRDAVKHKIKFSFMDLWGHVRGTGKLNFLVAEATYWKNDLGALE

NYLSKNTMTMSAFDPLHYNLYOASNSGNYDMRNLNLNGTLVORHPSHAVTFVDNHD

QPEALESQWGFKPLAYATILITREQGYPOVFGYDYGIPSDGVPSPYRQQIDPLILKA

ROQYAYGRQHDVFDHWDVIGMTREGNASHPNGLATIMSDGPGGSKWMTYVGROKAGEV

HHDMTGNRSYTVTINQDQWGHFFVNGSVSVWVKR"

BASE COUNT 439 a 293 c 365 g 361 t

ORIGIN

alignment\_scores:

Quality: 1905.50 Length: 483

Ratio: 4.411 Gaps: 2

Percent Similarity: 89.441 Percent Identity: 68.944

alignment\_block:

US-09-590-375-1 x AX037042 ..

Align seg 1/1 to: AX037042 from: 1 to: 1458

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

7 GATGGGACGAACGGAACGATTATGCGATTTTGAATGGAACGTTCCGAA 56

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

57 TGATGGACAAACATTGGAAACCGCTTACACAAACGCTCAAAATTTAAAAA 106

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

107 ATGCGCGAATTACAGCAATCTGGATTCCACCTGCGTGGAAAGGACGAGC 156

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

157 CAAAATGATGTAGCTACGGTGGCTATGACCTTTATGACCTTGCTGAATT 206

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

207 TAACCAAAAGGAACGGTCCGTACGAAATATGGAACAAAGCAGAAATTAG 256

84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

257 AACGAGCGATTTCGTTAAAGCGAACGGGATTCAAGTGTATGGCGAT 306

101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

307 GTTGTATGAACCAATAAAGCGGAGCTGATTTACCGAGCGGTGTTCAAGC 356

117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

357 GGTGGAAGTGAACCGCAAAACCGAAACCAAGAAAGTGTCTGGCACTTATC 406

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

407 AAATCGAAGCATGACAGGGTTCAATTTCTCGACGTGGCAATCAACAT 456

151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG1 167

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

457 TCTTCGTTTAAATGGCGCTGCTATCATTTTCGATGGGCGGATTGGGACCA 506

167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

507 GTCGCGCAACTCGCAATCTGATTTTATTAAGTTTAGAGGACGGAAG 556

182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

557 CATGGGACTGGGAAGTTGACACTGAAAATGGGAACATATGATTACTTAATG 606

198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

607 TATCGACAGCTTGACATCGATCCAGAGTGATTAACGAACATAACCG 656

214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

657 TTGGGGCTCTGGTACCGGAATACCTTAATTTAGACGGCTCCGACGTTG 706

231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

707 ATGCAGTGAACATATTAATTTAGCTTCATCGGTGATTGGTAGGGCAT 756

248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpPly 264

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

757 GTTCGCGGCAACGGGCAAGAATCTTTTTCGCTTGACAGAGTATTGGAA 806

264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

807 GAATGACCTAGGGCTTTAGAAAAATTTTAAAGCAAAACAAATTTGGACGA 856

281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

857 TGAGCGCCTTTGATGTTCCGCTTCATTACAACTTTTATCAAGCGTCAAT 906

298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG1 314

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

907 AGTAGCGAAATACGACATGAGAACTGTTAAATGGAACACACGCTTCA 956

314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

957 ACGTCATCCGAGCGATCGGTTTACGTTTGTTCGTAACCCACACACAGC 1006

331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1007 CTGAGAAGCCCTCGAATCGTTCGTTCAAGGCTGGTTTAAACCACTAGCT 1056

348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrG1 364

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1057 TATGCAACGATTTTACGAGAGACGAGCTACCCACCAAGTGTGTTTACGG 1106

364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1107 CGATTATTATGGCATCCCAAGTACGGTGTTCCAAGCTACCGTCAACAGA 1156





```

364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
1107 TCAGTACTATGAAATTCACACACATAGTGTCCACGCAATGAAAGCAAGA 1156

381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
1157 TTGATCCCAATCTTAGAGCGGTCAAAATTTTGCATATGGAACACAACAT 1206

398 AspTyrPheAspHisTyrAspValValGlyTyrThrArgGluGlySerSe 414
1207 GATTTATTTTGACCATCAATATATATATCGATGGACACAGTGAAGGAATAC 1256

414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
1257 CACGCATCCCAATTCAGGACTTGCAGCTATCATATGTCGGATGGCCAGGG 1306

431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
1307 GAGAGAAATGGATGTACAGTGGGCAAAATAAGCAGGTCAAGTTGGCAT 1356

448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
1357 GACATACTGGAAATAACCAGGACAGTACGATCAATGACAGATGGATG 1406

464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
1407 GGCTAATTTTTCAGTAATGGAGGATCTGTTCCATTTGGGTGAAACGA 1455

seq_name: gb_pat:AR049518
seq_documentation_block: 1455 bp DNA PAT 29-SEP-1999
LOCUS AR049518
DEFINITION Sequence 5 from patent US 5824531.
ACCESSION AR049518
VERSION AR049518.1 GI:6005557
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1455)
AUTHORS
Outtrup,H., Bisg.ang.rd-Frantzen,H., stergaard,P. Rahbek,
Rasmussen,M.Dolberg and Van der Zee,P.
TITLE
Alkaline bacillus amylase
JOURNAL
Patent: US 5824531-A 5 20-OCT-1998;
FEATURES
Location/Qualifiers
source
1..1455
/organism="unknown"
BASE COUNT 473 a 227 c 352 g 403 t
ORIGIN

alignment_scores:
Quality: 1860.50 Length: 483
Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

alignment_block:
US-09-590-375-1 x AR049518 ..
Align seg 1/1 to: AR049518 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTyrPheHisLeuGluAs 17
7 ANTGGACAATGGCGCATGATGCAATACTTTGAATGGCATTGCGCTAA 56

17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSera 34
57 TCGTGGAACTACTGGAATAGATTAAGAGATGATGCTAGTAACTAAGAA 106

34 sPalaglyIleThrAlaIleTrrIleProProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATACCGCTATTTGGATTCGCGCTGCGTGGAAAGGGACTTGG 156

```

```

51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAAATGATGGGTATGGAGCCTATGATCTTTATGATTAGGGGAATT 206

67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGCTAGTCAATTGG 256

84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGTCTGCCATCCATCGCTTTAAAGAAATATGGCGTTCAAGTTTATGGGAT 306

101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAACGTTCTTGC 356

117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 TGTCCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGGACTACA 406

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
407 CAATTGAGCTTGGACTAAGTTTGATTTTCCAGGAGGGGTAAATACATAC 456

151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
457 TCAGACTTTAAATGGCTGGTGTATCATTTTCGATGCTGTAGATTGGGATCA 506

167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 ATCAGCACAATTCAAAATCGTATCTACAAATTCGAGGTGATGTAAGG 556

182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
557 CATGGATGGGAGTGTAGTTCGGAAATGGAATATATGATTATTTAATG 606

198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGATGTAGATATGATCATCCGGAGGTAGTAAATAGCTTAGAAG 656

214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
657 ATGGGAGAAATGGTATACAAATACATTAATCTTGATGATTTAGGATCG 706

231 sPalIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATGCGGTGAGCATATTAATATAGCTTTACAGTGTGTTGGTCCCAT 756

248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
757 GTAAGAAACGCAACGGGAAAGAAATGTTGCTGTTGCTGAATTTTGGAA 806

264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
807 AAATGATTAGTGTGCTTGGAGAACTATTAAATAAAACAAACACTGGAATC 856

281 etSerLeuPheAspValProLeuAsnTyrAsnPhetyrArgAlaSerGln 297
857 ATTCGTCTTTGATGTCCCTTCATTAATATCTTTTAACCGCGTCAAT 906

298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValG 314
907 AGTGGAGGCAACTATGACATGCGCAAACTCTTAATGGAACGGTTGTCA 956

314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
957 AAAGCATCCAATGTCATGCGTAACCTTTTGTGATTAATCAGCATTCATCA 1006

331 roGlyGlySerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
1007 CTTGGGGAATCATTAGATTCATTGTACAAAGATGGTTTAAGCCACTTGT 1056

348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrG 364

```

1057 FATGCGCTATTTTAACAGAGACAAGGCTATCCCTCTCTCTCTATGG 1106  
||||| ||||||||| ||||||| : : : : : |||||||  
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381  
||||| : : : : : ||||| : : : : : |||||  
1107 TGACTACTATGGAATTCACACACATAGTGTGCCAGCAATGAAGCCAGA 1156  
||||| : : : : : ||||| : : : : : |||||  
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397  
||||| : : : : : ||||| : : : : : |||||  
1157 TTGATTCCAATCTTAGAGGCGCTCAAAATTTGCATATGGAACACACAT 1206  
||||| : : : : : ||||| : : : : : |||||  
398 AspTyrPheAspHisTrpAspValValClyTrpThrArgGluGlySerSe 414  
||||| : : : : : ||||| : : : : : |||||  
1207 GATTATTTTGACCATCATATAATATCGGATGGACACGCTGAAGGAATAC 1256  
||||| : : : : : ||||| : : : : : |||||  
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyC 431  
||||| : : : : : ||||| : : : : : |||||  
1257 CACGGATCCCAATTCAGACTTGGCAGCTATCATGTCGGATGGCCAGGG 1306  
||||| : : : : : ||||| : : : : : |||||  
431 LysrLysTrpMetTyrValClyArgGlnAsnAlaGlyGlnThrTrpThr 447  
||||| : : : : : ||||| : : : : : |||||  
1307 CAGAGAAATGGATGCTAGTAGGCGCAAAATAACAGGTCAAGTTTGGCAT 1356  
||||| : : : : : ||||| : : : : : |||||  
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464  
||||| : : : : : ||||| : : : : : |||||  
1357 GACATAACTGGAATAAACAGGAACAGTTTACGATCAATGCATGGATG 1406  
||||| : : : : : ||||| : : : : : |||||  
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480  
||||| : : : : : ||||| : : : : : |||||  
1407 GCCTAAATTTTCAGATAATGGAGATCTGTTTCCATTTGGTGAACAGA 1455  
||||| : : : : : ||||| : : : : : |||||

seq\_name: qb\_pat:AR104349

seq\_documentation\_block: 1455 bp DNA PAT 14-FEB-2001  
LOCUS AR104349 Sequence 5 from patent US 6093562.  
DEFINITION AR104349  
ACCESSION AR104349  
VERSION AR104349.1 GI:12817057

GENUS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1455)
AUTHORS	Bisg.ang.rd-Prantzen,H., Svendsen,A. and Borchert,T.Vedel.
TITLE	Amylase variants
JOURNAL	Patent: US 6093562-A 5 25-JUL-2000;
FEATURES	Location/Qualifiers
Source	1..1455 /organism="unknown"
BASE COUNT	473 a 227 c 352 g 403 t

alignment_scores:	
Quality:	1860.50
Ratio:	4.327
Percent Similarity:	89.027
Percent Identity:	66.460
Gaps:	2
Length:	483

alignment block:

US-09-590-375-1 x AR104349

Align seg 1/1 to: AR104349 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17  
::  
7 AATGGGCAAAATGGGACGATGAAGCAATCTTTGAATGGCATTGCCTAA 56  
::  
  
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA 34  
::  
57 TGTATGGGAATCACTGGNATAGANTAGAGAATGACTAGTAATCTAAGAA 106  
::  
  
34 spAlaGlyIleThrAlaIleTrpIleProProlatYrLysGlyAsnSer 50  
:: :

[illegible]



```

|||||CTGGGAATCAATTAGATCATTTGTACAGAATGTTTAAAGCCACTTGCT 1056
348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrGI 364
|||||TATCGGCTATTTTACAGACACAGGCTATCCCTGCTGCTTCTATGG 1106
364 yAspTyrTrpGlyIleProAsnAspAsnIleSerAlaIleLysAspMetI 381
1107 TGACTACTATGAATTCACACACATAGTGTCCACGAATGAAGCCCAAGA 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
1157 TTGATCCAACTTTAGAGCGCGTCAAAATTTTGTGATATGGAACAACAAT 1206
398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
1207 GATATATTTTGACCATCATATATATATCGGATGGACAGCTGAAGAAATAC 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
1257 CACGCATCCCAATTCAGGACTTGGACTATCATGTGCGATGGGCCAGGG 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
1307 GAGAGAATGGATGATGAGTGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
1357 GACATACTGGAATAAACACGAGAACAGTTACGATCAATGCAGATGGATG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
1407 GGTAAATTTTTCAGTAAATGAGGATCTGTTTCCATTTGGGTGAAACGA 1455
seq_name: gb_pat:AR129918

```

```

seq_documentation_block: 1455 bp DNA PAT 16-MAY-2001
LOCUS AR129918
DEFINITION Sequence 15 from patent US 6187576.
ACCESSION AR129918
VERSION AR129918.1 GI:14117815
KEYWORDS
SOURCE
ORGANISM

```

```

REFERENCE
1 (bases 1 to 1455)
AUTHORS Svendsen,A., Borchert,T,Vedel and Bisg.ang.rd-Frantzen,H.
TITLE .alpha.-amylase mutants
JOURNAL Patent: US 6187576-A 15 13-FEB-2001;
FEATURES
source
1..1455
/organism="unknown"
BASE COUNT 473 a 227 c 352 g 403 t
ORIGIN

```

```

alignment_scores:
Quality: 1860.50 Length: 483
Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

```

```

alignment_block:
US-09-590-375-1 x AR129918 ..

```

```

Align seg 1/1 to: AR129918 from: 1 to: 1455

```

```

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluas 17
...
7 AATGGACAATGGGAGGATGATGCAATACCTTTGATGGCAGCTTGCCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSera 34
|||||...

```

```

57 TGATGGCAATCACTGGAAATAGATTAAGAGATGATGCTAGTAATCTAAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50
...
107 ATAGAGTATAACCGCTATTGTGGATTCGCTGCTGCTGCTGCTGCTGCTGCTG 156
51 GluAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAAATCATGTGGGTATGAGCCTATGATCTTTATGATTTAGGGGAATT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGACACGCTAGTCAATTGG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGTCTGCATCCATGCTTTAAAGAATAATGCGCTTCAAGTTTATGGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTAGTGATGAACCAATAAGGAGGAGCTGATGCTACAGAAAACGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 TGTCGAGGTGAATCCAAATCAACGGAATCAAGAAATATCTGGGCACTACA 406
134 hrIleAspAlaTyrThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
407 CAATTGAGGCTTGACTAAGTTTTCAGGAGGAGGAGGATATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG 167
457 TCAGACTTTAAATGGCGTGGTATCATTTTCGATGCTGATGTTGGGATCA 506
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 ATCAGCACAATTCAAAATCGTATCTACAAAATTCGAGGTTGATGGTAAG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
557 CATGGGATTGGGAAGTAGATTCGAAAATGGAATATGATTTAATTAATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGATGTAGATATGATATCGGAGGTAGTAAATGAGCTTAGAAG 656
214 pTrpGlySerTrpPheTrpAspGluLeuAspLeuAspGlyTyrArgLeuA 231
657 ATGGGAGATGTGTATACAAATACATTAATCTTGATGATTTAGGATCG 706
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATCGCGTGAAGCATATTAATATAGCTTTACACGCTGATGTTGGTACCCT 756
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
757 GTAAGAAACGCAACACGGAAGAAATGTTGCTGTTGCTGAATTTTGGA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGlu 281
807 AATGATTTAGTGCTTGGAGAACTATTTAAATAAAACAACTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 ATTCTGCTCTTGTATGCCCTTCATTATAATCTTTATAACGCGTCAAA 906
298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl 314
907 AGTGGAGGCAACTATGACATGCGCAAACTTCTTAATGGAACGCTGTCTCA 956
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
957 AAAGCATCAATGCATGCCGTAACTTTTGGGTAATACAGATTCCTCAAC 1006

```

```

331  roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1007 CTGGGAATCATTAGAAATCTGTACAAAGATGGTTTAAGCCACTTGCT 1056

348  TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGI 364
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1057 TATGCCCTATTATTAAACAGAGAACAAGGCTATCCCTCTCTCTCTATGG 1106

364  yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1107 TGACTACTATGNAATCCAAACACATAGTCTCCAGCAATCAAGCCCAAGA 1156

381  leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1157 TTGATCCAATCTTAGAGCGCGCTCAAAATTTTGCATATGGAACACAACAT 1206

398  AspTyrPheAspHisTrpAspValValGlyTyrThrArgGluGlySerSe 414
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1207 GATTATTTTGACCATCATATAATATCGGATGGACACACGCTGAAGGAATATC 1256

414  rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1257 CAGCGATCCCAATTCAGACTTGGCGACTATCATGTCGATGGGCCAGGGG 1306

431  lysSerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1307 GAGAGAAATGGATGTACGTAGGCGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356

448  AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTyr 464
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1357 GACATAACTGGAAATAAACCAGGAACAGTTACGATCAATGCAGATGGATG 1406

464  pGlyGluPhePheThrAsnGlyGlySerValSerValThrValAsnGln 480
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1407 GGTCAATTTTCAGTAATAGGAGGACTCTGTTCCATTTGGGTGAAACGA 1455

```

seq\_name: gb\_pat:AR137884

```

seq_documentation_block:
LOCUS AR137884 1455 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 10 from patent US 6197565.
ACCESSION AR137884
VERSION AR137884.1 GI:14479393
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1455)
AUTHORS Svendsen,A., Kjaerulff,S., Bisgaard-Frantzen,H. and Andersen,C.
TITLE .alpha.-Amylase variants
JOURNAL Patent: US 6197565-A 10 06-MAR-2001;
FEATURES
source Location/Qualifiers
1..1455 /organism="unknown"
BASE COUNT 473 a 227 c 352 g 403 t
ORIGIN

```

```

alignment_scores:
Quality: 1860.50 Length: 483
Ratio: 4.327 Gaps: 2
Percent Similarity: 89.027 Percent Identity: 66.460

```

alignment\_block:

US-09-590-375-1 x AR137884

Align seg 1/1 to: AR137884 from: 1 to: 1455

```

1  AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
7  ATGGGCAAAATGGGAGCATGATGCATCTTTGGAATGGCACTTGCTCTAA 56

```

```

17  nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
57  TGATGGGAATCACTGCAATAGATTAAGAGATGATGCTAGTAATCTAAGAA 106

34  spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
::: :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
107 ATAGAGGTATTAACCGCTATTGTGATTCCCGCTCCCTCGGAAGGCACTTCG 156

51  GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
157 CAAATATGATGTGGGGTATGGAGCTATGATCTTTATGATTTAGGGGAATT 206

67  eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
207 TAATCAAAAGGGGACGCTTCTACTAAGTATGGACACGCTAGTCAATTGG 256

84  luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
|| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
257 AGTCTGCCATCCATGCTTTAAAGAAATAATGGCGTTCAAGTTTATGGGAT 306

101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
307 GTAGTGATGAACCATTAAGAGGAGGCTGATGCTACAGAAAACGTTCTTGC 356

117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
357 TGTGAGGTTGAATCCAAATCAACCGGAATCAAGAAATATCTCGGGACTACA 406

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
407 CAATTGAGGCTTGGACTAAGTTTGATTTCCAGGAGGGGTAATACATAC 456

151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGI 167
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
457 TCAGACTTTAAATGGCGTGGTGTATCATTTTCGATGGTGTAGATTGGGATCA 506

167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
|| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
507 ATCAGCACAATTCCAAATCGTATCTACAAATTCAGAGGTGATGGTAAGG 556

182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
557 CATGGGATTTGGGAAGTAGATTCCGAAATATGAAATATGATATTATTAAATG 606

198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
::: :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
607 TATGCAGATGTAGATATGATGATCATCGGAGGTAGTAATAGCTTAGAAG 656

214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
657 ATGGGGAATGCTATACAAATACATTAATCTTGATGGATTATTAGGATCG 706

231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
707 ATCGGTGAAGCATATTAATATAGCTTTACACGTGATTGTTGATGCCCAT 756

248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGlyTyrTrpLy 264
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
757 GTAAGAAACCCCAACGGGAAAGAAATGTTGCTGCTGAATTTGGAA 806

264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
::: :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
807 AAATGATTTAGGTGCCTTGGAGAACTATTTAAATAAAACAAACCTGGAATC 856

281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
857 ATTCTGCTCTTTGATGTCCTCCCTTCATTATAATCTTTATACCGCTCAAAAT 906

298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGI 314
::: :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
907 AGTGGAGGCAACTATGACATGGCAAACTCTTTAATGGAACGGTGTGTCA 956

314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331

```

```

1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818 2819 2820 2821 2822 2823 2824 2825 2826 2827 2828 2829 2830 2831 2832 2833 2834 2835 2836 2837 2838 2839 2840 2841 2842 2843 2844 2845 2846 2847 2848 2849 2850 2851 2852 2853 2854 2855 2856 2857 2858 2859 2860 2861 2862 2863 2864 2865 2866 2867 2868 2869 2870 2871 2872 2873 2874 2875 2876 2877 2878 2879 2880 2881 2882 2883 2884 2885 2886 2887 2888 2889 2890 2891 2892 2893 2894 2895 2896 2897 2898 2899 2900 2901 2902 2903 2904 2905 2906 2907 2908 2909 2910 2911 2912 2913 2914 2915 2916 2917 2918 2919 2920 2921 2922 2923 2924 2925 2926 2927 2928 2929 2930 2931 2932 2933 2934 2935 2936 2937 2938 2939 2940 2941 2942 2943 2944 2945 2946 2947 2948 2949 2950 2951 2952 2953 2954 2955 2956 2957 2958 2959 2960 2961 2962 2963 2964 2965 2966 2967 2968 2969 2970 2971 2972 2973 2974 2975 2976 2977 2978 2979 2980 2981 2982 2983 2984 2985 2986 2987 2988 2989 2990 2991 2992 2993 2994 2995 2996 2997 2998 2999 3000 3001 3002 3003 3004 3005 3006 3007 3008 3009 3010 3011 3012 3013 3014 3015 3016 3017 3018 3019 3020 3021 3022 3023 3024 3025 3026 3027 3028 3029 3030 3031 3032 3033 3034 3035 3036 3037 3038 3039 3040 3041 3042 3043 3044 3045 3046 3047 3048 3049 3050 3051 3052 3053 3054 3055 3056 3057 3058 3059 3060 3061 3062 3063 3064 3065 3066 3067 3068 3069 3070 3071 3072 3073 3074 3075 3076 3077 3078 3079 3080 3081 3082 3083 3084 3085 3086 3087 3088 3089 3090 3091 3092 3093 3094 3095 3096 3097 3098 3099 3100 3101 3102 3103 3104 3105 3106 3107 3108 3109 3110 3111 3112 3113 3114 3115 3116 3117 3118 3119 3120 3121 3122 3123 3124 3125 3126 3127 3128 3129 3130 3131 3132 3133 3134 3135 3136 3137 3138 3139 3140 3141 3142 3143 3144 3145 3146 3147 3148 3149 3150 3151 3152 3153 3154 3155 3156 3157 3158 3159 3160 3161 3162 3163 3164 3165 3166 3167 3168 3169 3170 3171 3172 3173 3174 3175 3176 3177 3178 3179 3180 3181 3182 3183 3184 3185 3186 3187 3188 3189 3190 3191 3192 3193 3194 3195 3196 3197 3198 3199 3200 3201 3202 3203 3204 3205 3206 3207 3208 3209 3210 3211 3212 3213 3214 3215 3216 3217 3218 3219 3220 3221 3222 3223 3224 3225 3226 3227 3228 3229 3230 3231 3232 3233 3234 3235 3236 3237 3238 3239 3240 3241 3242 3243 3244 3245 3246 3247 3248 3249 3250 3251 3252 3253 3254 3255 3256 3257 3258 3259 3260 3261 3262 3263 3264 3265 3266 3267 3268 3269 3270 3271 3272 3273 3274 3275 3276 3277 3278 3279 3280 3281 3282 3283 3284 3285 3286 3287 3288 3289 3290 3291 3292 3293 3294 3295 3296 3297 3298 3299 3300 3301 3302 3303 3304 3305 3306 3307 3308 3309 3310 3311 3312 3313 3314 3315 3316 3317 3318 3319 3320 3321 3322 3323 3324 3325 3326 3327 3328 3329 3330 3331 3332 3333 3334 3335 3336 3337 3338 3339 3340 3341 3342 3343 3344 3345 3346 3347 3348 3349 3350 3351 3352 3353 3354 3355 3356 3357 3358 3359 3360 3361 3362 3363 3364 3365 3366 3367 3368 3369 3370 3371 3372 3373 3374 3375 3376 3377 3378 3379 3380 3381 3382 3383 3384 3385 3386 3387 3388 3389 3390 3391 3392 3393 3394 3395 3396 3397 3398 3399 3400 3401 3402 3403 3404 3405 3406 3407 3408 3409 3410 3411 3412 3413 3414 3415 3416 3417 3418 3419 3420 3421 3422 3423 3424 3425 3426 3427 3428 3429 3430 3431 3432 3433 3434 3435 3436 3437 3438 3439 3440 3441 3442 3443 3444 3445 3446 3447 3448 3449 3450 3
```

```

314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
957 AAAGCATCAATGCGTAACTTTGTGGTAATCAGGATTCCTCAAC 1006

331 rGlyCylSerLeuGluSerTrpValAlaAspTrpPheLeuAla 347
1007 CTTGGGAATCATAGATCATTTGTACAGAAATGTTTAAAGCACTTGGT 1056

348 TyrAlaThrIleLeuThrArgGluGlyTyrProAsnValPheTyrGl 364
1057 TATGGCGCTATTATTAACAGACAGACAGCTATCCCTCTGCTTCTATGG 1106

364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
1107 TGACTACTATGAAATTCACACACATAGTGTCCAGCAATGAAGCCAAGA 1156

381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
1157 TTGATCCCAATCTAGAGCGCGTCAAAATTTTGCATATGGAACACAACAT 1206

398 AspTyrPheAspHisTrpAspValValGlyTyrTrpThrArgGluGlySerSe 414
1207 GATTATTTTGACCATCATATAATATATCGATGGACACGCTGAAGGAATAC 1256

414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
1257 CACGCATCCCAATTCAGGACTTCGACATATCATGTCGGATGGCCAGGG 1306

431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
1307 GAGAGAAATGGATGTACGTAGGCGCAAAATAAAGCAGGTCAAGTTGGCAT 1356

448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
1357 GACATACTGGAAATAAACCGAAGACAGTTACGATCAATGTCAGATGGATG 1406

464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
1407 GGCTAATTTTCAGTAATGAGGATCTGTTCCATTGTTGGGTGAACGA 1455

```

seq\_name: gb\_pat:AR143214

```

seq_documentation_block:
LOCUS AR143214 1455 bp DNA PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6204232.
ACCESSION AR143214
VERSION AR143214.1 GI:15104500

```

## KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1455)

## AUTHORS

Borchert,T.Vedel, Svendsen,A., Andersen,C., Nielsen,B.,

Nissen,T.Lauesgaard and KJ.ae buttet.rulff,ssliashedren.

## TITLE

alpha.-amlase mutants

## JOURNAL

Patent: US 6204232-A 10 20-MAR-2001;

## FEATURES

Location/Qualifiers

source

1..1455

/organism="unknown"

BASE COUNT 473 a 227 c 352 g 403 t

## ORIGIN

## alignment\_scores:

Quality: 1860.50 Length: 483

Ratio: 4.327 Gaps: 2

Percent Similarity: 89.027 Percent Identity: 66.460

## alignment\_block:

US-09-590-375-1 x AR143214 ..

Align seg 1/1 to: AR143214 from: 1 to: 1455

```

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
7 ANTGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTTCCTCAA 56

17 nAspGlyGlnHisTrpAsnArgLeuHisAspAlaAlaLeuSerA 34
57 TCATGGGAATCACTGGAATAGATTAAAGAGATGATGCTAGTAATCAAGAA 106

34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50
107 ATAGAGGTATAACCGCTATTGGATTCCCGCTGCGCTGGAAAGGAGACTCG 156

51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
157 CAAATGATGTGGGTATGAGCCATATGATCTTTATGATTTAGGGGAATT 206

67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
207 TAATCAAAAGGGGACGGTTTCGTACTAAGTATGGACACGCTAGTCAATTGG 256

84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
257 AGTCTGCCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTTATGGGAT 306

101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
307 GTAGTGATCAACCAATAAAGGAGGAGCTGATCTACAGAAACGTTCTTGC 356

117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
357 TGTCTGAGGTGAATCCAAATTAACCGAATCAAGAAATATCTGGGCACTACA 406

134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
407 CAATTGAGGCTTGGACTAAGTTTGATTTCAGGGAGGGGTATACATAC 456

151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
457 TCAGACTTTTAAATGCGTTGGTATCATCTTCGATGGTGTAGATTGGGATCA 506

167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
507 ATCAGCACAATTCACAAATTCGTATCTACAAATTCGAGGATGATGGTAAG 556

182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
557 CATGGATTGGGAAGTAGATTTCGAAATGGAATGGAATATATGATTATTATG 606

198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
607 TATGCAGATGTAGATATGATCGGAGGTAGTAATAGCTTAGAAG 656

214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
657 ATGGGAGAATGGTATACAAATTAATCTTCATGGATTAGGATCG 706

231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
707 ATGCGGTGAAGCATATTAATATATGCTTTACACGTGATTGGTTGACCCAT 756

248 GlnArgAsnGlnAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
757 GTAAGNAACGCAACGGGAAAGAAATGTTGCTGTGCTGAATTTGGAA 806

264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
807 AAATGATTAGGTGCGCTTGGAGAACTATTTAAATAAAACAAACACTGGAATC 856

281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
857 ATTCTGTCTTGTATGTCGCCCTTCATTATAATCTTTTATAACGCGTCAAT 906

```

```

298 GlnGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl 314
   ::::::::::::::::::::
907 AGTGGAGCAACTATGACATGCGCAAACTCTAATGGAAACGGTTGTCCA 956
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
   : ::::::::::::::::::::
957 AAGCATCAATGATGCGGTAACTTTTGTGGATATACAGATTCTCAAC 1006
331 roGlySerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
   ::::::::::::::::::::
1007 CTGGGAATCATTAAGATCTTTTACAAAGATGTTTAAAGCCACTTGTCT 1056
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl 364
   ::::::::::::::::::::
1057 TATGCGCTTATTTTAAAGAGAACAGCGCTATCCTCTGCTCTCTATGG 1106
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
   ::::::::::::::::::::
1107 TGACTACTATGGAATTCACACATAGTGTCCAGCAATGAAAGCCAAG 1156
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
   ::::::::::::::::::::
1157 TTGATCCCAATCTTAGAGCGCGCTCAAAATTTTGCATATGGAAACACA 1206
398 AspTyrPheAspHisTrpAspValValGlyTyrTrpThrArgGlySerSe 414
   ::::::::::::::::::::
1207 GATTATTTTGACCATCATATAATATATCGATGGACGTCGAAGGAATAC 1256
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
   ::::::::::::::::::::
1257 CACGATCCCAATTCAGGACTTGGGACTATCATCTCGGATGGGCGAGGG 1306
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
   ::::::::::::::::::::
1307 GAGAGAAATGGATCTAGTAGGGCAAAATAAAGCAGGTCAAGTTGGCAT 1356
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
   ::::::::::::::::::::
1357 GACATAACTGGAATAAACAGGAAACAGTTACGATCAATGCAGATGGATG 1406
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
   ::::::::::::::::::::
1407 GGCTAATTTTCAGTAATGAGGAGTCTGTTCCATTTGGGTGAACGA 1455

```

seq\_name: gb\_pat:AR143218

seq\_documentation\_block: 1455 bp DNA PAT 08-AUG-2001  
 LOCUS AR143218  
 DEFINITION Sequence 14 from patent US 6204232.  
 ACCESSION AR143218  
 VERSION AR143218.1 GI:15104504

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 1455)

AUTHORS

Borchert,T.Vedel, Svendsen,A., Andersen,C., Nielsen,B.,

Nissen,T.Lauegaard and Kj.ae buttet.ruliff.Sslashedren.

TITLE

.alpha.-amylase mutants

JOURNAL

Patent: US 6204232-A 14 20-MAR-2001;

FEATURES

Location/Qualifiers

1..1455

/organism="unknown"

BASE COUNT 473 a 227 c 352 g 403 t

ORIGIN

alignment\_scores:

Quality: 1860.50 Length: 483

Ratio: 4.327 Gaps: 2

Percent Similarity: 89.027 Percent Identity: 66.460

.alignment\_block:

```

US-09-590-375-1 x AR143218 ..
Align seg 1/1 to: AR143218 from: 1 to: 1455

1 AspGlyLeuAsnGlyThrMetGlnTyrTyrGluTrpHisLeuGluAs 17
   ::::::::::::::::::::
7 AATGGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTTGCCTAA 56
17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA 34
   ::::::::::::::::::::
57 TGATGGGAATCACTGGATAGATTAAGATGATGCTAGTAATCTAAGAA 106
34 spAlaGlyIleThrAlaIleTrpIleProAlaTyrLysGlyAsnSer 50
   ::::::::::::::::::::
107 ATAGAGGTATAACCGCTATTGTGGATTCCGCTGCTGCTGAAAGGACTCG 156
51 GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
   ::::::::::::::::::::
157 CAAATGATGTGGGTATGGAGCCTATGATCTTTATGATTTAGGGGAATT 206
67 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84
   ::::::::::::::::::::
207 TAATCAAAAGGGGACGCTTCGTACTAAGTATGGACACGTAAGTCAATTG 256
84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
   ::::::::::::::::::::
257 AGTGTCCATCCATCGCTTTAAAGAAATAATGCGCTTCAAGTTTATGGGAT 306
101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
   ::::::::::::::::::::
307 GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAACCGTTCTTGC 356
117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
   ::::::::::::::::::::
357 TGTGCGAGGTGAATCCAAATAAACCGGAATCAAGAAATATCTGGGACTACA 406
134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
   ::::::::::::::::::::
407 CAATTGAGGCTTGGACTAAGTTTATGATTTCCAGGAGGAGGTAATACATAC 456
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
   ::::::::::::::::::::
457 TCAGACTTTAAATGGCGTGGTATCATTTTCGATGGTGTAGATTGGGATCA 506
167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn... 181
   ::::::::::::::::::::
507 ATCAGCACAATTCCAAATTCGTATCTACAAATTCGAGGAGGTGTAAGG 556
182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
   ::::::::::::::::::::
557 CATGGGATTGGGAAGTAGATTCGAAAAATGGAAATTTATGATTATTAAATG 606
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
   ::::::::::::::::::::
607 TATCGAGATGATAGATATGATCATCCGAGGAGTAGTAAATGAGCTAGAAG 656
214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
   ::::::::::::::::::::
657 ATGGGGAAGATGATACAAATACATTAATCTCTGATGATTAGGATCG 706
231 spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247
   ::::::::::::::::::::
707 ATGCGGTGAAGCATATTAATAATAGCTTTTACACGTGATTTGGTGGCCAT 756
248 GlnArgAsnGluAlaAspClnAspLeuPheValValGlyGluTyrTrpLy 264
   ::::::::::::::::::::
757 GTAAGAAACGCAACGGGAAAGAAATGTTTGTCTTGTCTGAATTTTGGAA 806
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
   ::::::::::::::::::::
807 AAATGATTAGTGTGGAGAACTATTTAATAATAAACAACTGGAATC 856
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297

```



[illegible]

```

34  spAlaGlyIleThrAlaIleTrpIleProProAlaIleLysGlyAsnSer 50
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
344  GTAAGGGATTACCGCTCTTGGGATTCCTCGTCGATGGAAGGGGACTTCG 393
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  GlnAlaAspValGlyThrGlyAlaIleThrAspLeuValGlyGluPh 67
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
394  CAATATGATGTTGGGTATGGTCCCTATGATTGTACGATCTTGGTGAGTT 443
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  eAsnGlnLysGlyThrValArgThrLysThrGlyThrLysAlaGlnLeuG 84
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
444  TAACCAAAAGGGAACCGCTCCGTACAAAAATATGGCAACAGGAGTCAGTTGC 493
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84  luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValThrGlyAsp 100
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
494  AAGTGCGCGTGACATCTTTGAAAATAACCGGATTCAGTTATGGGGAT 543
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101  ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
544  GTCGTGATGAATCATAAAGGTGGAGCACACCGGCAGAGATGGTAAATGC 593
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117  aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaIleTyr 134
   :  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
594  GGTGGAGTGAAACCAAGCAACCGCAAAACCAAGAAATATCAGTGAATACA 643

```

```
134 hrLleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
644 CCATTGAAGCATGGAGAAATTTGATTTTCCTCGGAGAGGAAATACCCAT 693
151 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspG1 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
694 TCCAACTTTAAATGGCGCTGGTATCATTTTGTATGGGACAGATTGGGATCA 743
167 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn... 181
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
744 GTCACGTCAGCTTCAGACAAATATATAAATTCAGAGGTACCGGAAAGG 793
182 ..TrpAsnTrpArgValAspGluAsnGlyAsnTyrAspTyrLeuLeu 197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
794 CATGGGACTGGGAAGTAGATATAGAACGCAACGCAATATGATTACCTTATG 843
198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
844 TATGCAGACATTGATGGATCATCCAGAAAGTAAATCAATGAATCTAGAAA 893
214 pTrpGlySerTrpPheTrpThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
894 TTGGGGAGTTGGTATACAAATACACTTAATCTAGATGGATTAGAAATCG 943
231 splalLysHisIleProPheTrpTrpThrSerAspTrpValArgHis 247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
944 ATGCTGTGAACATATATAATACAGCTATACGAGAGATTGGCTAACACAT 993
248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTrpTrpLys 264
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
994 GTGGGTACACACAGGTAAACCAAGTTTGGCAGTTGCAGAAATTTGGAA 1043
264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1044 AAATGACCTTGTGCAATCGAAACATATTATAATAAAACAAGTTGGAATC 1093
281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1094 ACTCCGGTGTTCGATGTTCCCTCTTCAATATATATTTGTACAATGCAATCA 1143
298 GlnGlyLysSerTyrAspMetArgAsnIleLeuArgGlySerLeuValG1 314
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1144 AGTGGTGGCTATTTTGATATGAGAAATATTTTAAATGCTTCTGCTGAC 1193
314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1194 AAAACACCTTATACATCGATCAGTCACATTTGTTGATAACCATGACTCTCAGC 1243
331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1244 CAGGAGAAGCATTTGGAATCCTTTGTTCAATCGTGGTTCAAACACCATCGCA 1293
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrG1 364
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1294 TATGCATTGATTCGACAAAGGACCAAGTTTACCCTTCCGTTATTTACGG 1343
364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1344 TGATTACTACGTTATACCAATCATGCTGTTCCCTTCGATGAAATCTATAAA 1393
381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1394 TTGATCCACTTCTCGAGCGAGTCAAAAGTATGCTACGGAACCCAAACAT 1443
398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1444 GATTATTTTGCATCATGATATATATATCGCTGGACGAGAGAGAGGGGACAG 1493
414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1494 CTCGCCCAAAATTCAGGACTTGCACACTATATATGTCGATGGGCGCAGGG 1543
431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
```

```
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1544 GTAATAAATGGATGTATCGGGAAACATAAAGCTGGCCAAGTATGAGA 1593
448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1594 GATATCACCGGAATAGGCTGCTACCGTCACCATTAATGCAGATGGTTG 1643
464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1644 GGGGAATTTCACTGTAAACGAGGCGAGTTTCGGTTTGGTGAAGCAA 1692
```

seq\_name: gb\_ba:AB008763

seq\_documentation\_block: 1786 bp DNA BCT 21-AUG-1998

LOCUS AB008763 Bacillus sp. gene for amylase, complete cds.

DEFINITION AB008763

ACCESSION AB008763

VERSION AB008763.1 GI:3445479

KEYWORDS amylase.

ORGANISM Bacillus sp. (strain:KSM-1378) DNA.

SOURCE Bacillus sp.

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Bacillus.

REFERENCE 1 (bases 1 to 1786)

AUTHORS Hatada,Y.

TITLE Direct Submission

JOURNAL Submitted (10-NOV-1997) to the DBJ/EMBL/GenBank databases. Yuji

Hatada, Kao Corporation, Toehigi Research Laboratories; 2606

Akabane, Ichikai, Haga-gun, Tochigi 321-3497, Japan

(Tel:0285-68-7400, Fax:0285-68-7403)

REFERENCE 2 (bases 1 to 1786)

AUTHORS Igarashi,K., Hatada,Y., Ikawa,K., Araki,H., Ozawa,T., Kobayashi,T.,

Ozaki,K. and Ito,S.

TITLE Improved thermostability of a Bacillus alpha-amylase by deletion of

an arginine-glycine residue is caused by enhanced calcium binding

JOURNAL Biochem. Biophys. Res. Commun. 248 (2), 372-377 (1998)

MEDLINE 98342096

FEATURES

source

1..1786

/organism="Bacillus sp."

/strain="KSM-1378"

/db\_xref="taxon:1409"

155..1705

/codon\_start=1

/transl\_table=11

/product="amylase"

/protein\_id="BAA32431.1"

/db\_xref="GI:3445480"

/translation="MKLHNRIISVLLTLLAVAVLPYMTPEAQAHNNGTNGTMMQYF

EWHLPNDGNHNRNLRDDAANLKSIGITAVWIPPAWKPQNDVGYGAYDLYDLGFNQ

KGTVRTKYSQLOGAVTSLKNNGIQVIGDVVMNHKGGADGTEMVAVENRNRNQ

EISGEYTIKATKFDPPGRTNHSFKRWYHFDGTDWDQSLQNKIKYKFGTKAW

DWEVDIENGNDYLMYADIDMDHPEVINELRNWVYTTNLNLDGFRIDAVKHISY

TRDLWTHVRNTTGGKPMFAVEFKNDLAAIENYLNKTSWNHSVFDVPLHYNLNASNS

GGYFDNRNLLGSSVVKQHPHIAVTFVDNHDSDOPGALSFVGSFWEKPLAYALITREQ

GYPSVFGDYGIPTHPGSPMSKIDPLLOARQYAYGTOHDYFDHDDHIGWTRGDS

SHPNGLGLRITSDSGPGGNKMWIVGAKHAGQVWRDITGNRSQVITINADGWGNFTVNGG

BASE COUNT 578 a 307 c 420 g 481 t

ORIGIN

alignment\_scores:

Quality: 1853.50

Ratio: 4.300

Percent Similarity: 89.234

Length: 483

Gaps: 2

Percent Identity: 66.874

alignment\_block:

US-09-375-1 x AB008763 ..

Align seg 1/1 to: AB008763 from: 1 to: 1786

1 AspGlyLeuAsnGlyThrMetMetGlnTyrGluTrpHisLeuGluAs 17

1154 AGTGGTGCGCTATTTTCATATGAGAAATATTAAAAATGGTCTGTCCGTACA 1203

314 ualHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1204 AAAACCCCATATACATGCAGTCACATTTGTTGTAATAACCACACTCTCAGC 1253

331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1254 CAGGAGAAGCAATGGAATCCCTTTGTTCAATCGTGGTTCAAACCACTGGCA 1303

348 TyrAlaThrIleLeuThrArgGluGlyTyrrProAsnValPheTyrrGl 364  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1304 TATGCATTGATTCTCACAAAGGAGCAAGTTACCTTCCGTATTATTACGG 1353

364 yAspTyrrTyrrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1354 TGATTACTACGGTATACCAACTCATGGTGTCTTCGATGAAATCTAAAAA 1403

381 leAspGluLeuLeuAspAlaArgGlnAsnTyrrAlaTyrrGlyThrGlnHis 397  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1404 TTGATGCCACTTCTCGACGACGCTCAAAAGCTATGCTACGGAACCCAACAT 1453

398 AspTyrrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1454 GATTATTGTGATCATCATGATATTATCGCTGGACGAGAGAAGGGGACAG 1503

414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG 431  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1504 CTCCCACCCAAAATTCAGGACTTGCAACTATTATGTCCGATGGCGCAGGG 1553

431 lySerLystrpMetTyrrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1554 GTAAATAATGGATGTATGTCGGGAACAATAAAGCTGGCCAAGTAGTGAGA 1603

448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyYr 464  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1604 GATATCACCGGAAATAGGTCTGGTACCGTCCACATTATATGCAGATGGTGTG 1653

464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrrValAsnGln 480  
: |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
1654 GGGAATTTCACTGTAAACGAGGAGGGCAGTTTCGGTTTTGGGTGAAGCAA 1702

**THIS PAGE BLANK (USPTO)**